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(54) **GENOMIC MARKERS FOR PREDICTION OF LONG-TERM RESPONSE TO 2 YEARS OF GROWTH HORMONE (GH) THERAPY**

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None
See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to the use of genetic markers to identify the response to growth hormone treatment in Growth Hormone Deficiency (GHD) or Turner Syndrome (TS) patients as well as a method of treating GHD or TS patients and kits for genotyping.

2 Claims, No Drawings

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GENOMIC MARKERS FOR PREDICTION OF LONG-TERM RESPONSE TO 2 YEARS OF GROWTH HORMONE (GH) THERAPY

CROSS-REFERENCE TO RELATED APPLICATION

This application is the U.S. national stage application of International Patent Application No. PCT/EP2012/058636, filed May 10, 2012.

FIELD OF THE INVENTION

The present invention relates, generally, to pharmacogenetics, more specifically to genetic markers associated with the clinical response to Growth Hormone in Growth Hormone Deficiency (GHD) or Turner Syndrome (TS). The present invention more particularly relates to human genes, which can be used for the diagnosis and treatment of Growth Hormone Deficiency (GHD) or Turner Syndrome (TS).

The invention further discloses specific polymorphisms or alleles of several genes that are related to GHD or TS response to second year of GH treatment as well as diagnostic tools and kits based on these susceptibility alterations. Thus, the invention can be used in the diagnosis or detection of the presence, risk or predisposition to, as well as in the prevention and/or treatment of GHD or TS and in predicting the response to growth hormone (GH) treatment.

BACKGROUND OF THE INVENTION

Growth Hormone Deficiency (GHD) includes a group of different pathologies all with a failure or reduction of growth hormone (GH) secretion. GHD may occur by itself or in combination with other pituitary hormone deficiencies. It may be congenital or acquired as a result of trauma, infiltrations, tumour or radiation therapy. Despite the large number of possible aetiologies, most children have idiopathic GHD. Depending on the criteria for diagnosis, the incidence of short stature associated with severe childhood GHD has been estimated to range between 1:4000 to 1:10000 live children in several studies (P C Sizonenko et al., Growth Horm IGF Res 2001; 11(3):137-165).

Postnatal growth of children with GHD differs according to aetiology. Genetic deficiency of GHD causes progressive slowing of growth following normal growth in the first months of life. Growth failure is the major presenting sign of GHD in children, and lack of GH therapy in the case of severe GHD leads to very short stature in adulthood (GH Research Society, J. Clin. Endocrinol Metabol 2000; 85(11): 3990-3993).

Turner (or Ullrich-Turner) syndrome (TS) is a chromosomal abnormality characterized by the absence of the entire chromosome X or a deletion within that chromosome. TS affects one in 1,500 to 2,500 live-born females. Short stature and reduced final height are observed in 95% of girls with TS. The average difference between mean adult height of normal women and that of TS adults is of 20 cm (Park E. et al, Pediatr Res 1983; 17:1-7). Reduced final height is due to a decline in height velocity after the age of 5 or 6 years (relative to unaffected girls) and to the absence of a pubertal growth spurt (Brook C G D et al., Arch Dis Child 1974; 49:789-795) due to the lack of the normal increase in GH secretion observed during puberty. The short stature in TS is not attributable to deficient secretions of GH or insulin-like growth factor I (IGF-I) (Cutler L et al., J Clin Endocrinol Metab 1985; 60:1087-1092), but a decreased amplitude and frequency of

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GH pulses have been reported after the age of 8 years in these patients (Ross J L et al., J Pediatr 1985; 106:202-206).

Recombinant DNA-derived human growth hormone (rhGH) is the only drug approved specifically for treatment of childhood growth failure and short stature, such as GHD, SGA (Small for Gestational Age) and TS. Current dose regimens for childhood GH therapy are based on body weight and are derived primarily from empirical experience. Variability in individual growth response to weight-based dosing in pediatric indications has led to a search for methods to optimise dosing based on other physiologic parameters. Models for prediction of GH treatment response have thus far relied on biochemical, demographic and anthropometric measures and can account for up to ~70% and ~40% of the first and second-year growth respectively in response to rhGH.

However, the potential additional effects of genetic variability have not been fully explored. There is thus a need to define a set of genetic/genomic markers associated with short term GH treatment response that could complement the previously identified auxological and biochemical parameters to increase the accuracy with which response to GH treatment could be predicted.

SUMMARY OF THE INVENTION

According to one aspect of the invention, a method is provided for identifying in an individual suffering from Growth Hormone Deficiency or Turner Syndrome, the level of response after the second year of treatment, using annualized clinical endpoints related to the efficacy of growth hormone treatment.

According to another aspect of the invention, a method is provided for treating Growth Hormone Deficiency or Turner Syndrome comprising genotyping the Growth Hormone Deficiency or Turner Syndrome patient and adjusting treatment of the Growth Hormone Deficiency or Turner Syndrome patient based upon the results of the genotyping.

According to another aspect of the invention, a kit is provided for detecting a genetic marker or a combination of genetic markers that is or are associated with the level of response to the second year of growth hormone treatment in an individual suffering from Growth Hormone Deficiency or Turner Syndrome.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides novel approaches to the detection, diagnosis and monitoring of GHD and TS in a subject, as well as for genotyping of patients having GHD or TS. The invention further provides novel approaches to the treatment of GHD and TS in a subject, and to predicting the response to growth hormone (GH) treatment thereby enabling the adjustment of the necessary dose of GH in a patient individualized manner.

Current medications to stimulate linear growth with GH in GHD and TS include SAIZEN®. The active ingredient of SAIZEN® is somatropin, a recombinant human growth hormone (rhGH) produced by genetically engineered mammalian cells (mouse C127). Somatropin is a single-chain, non-glycosylated protein of 191 amino acids with two disulphide bridges.

SAIZEN® is registered in many regions in the following paediatric indications:

- growth failure in children caused by decreased or absent secretion of endogenous growth hormone
- growth failure in children due to causes other than GHD (Turner Syndrome, growth disturbance in short children born SGA)
- growth failure in prepubertal children due to chronic renal failure.

SAIZEN® is also registered in 42 countries, including 15 European countries and Switzerland, in the indication of “pronounced growth hormone deficiency” in the adult.

The term “growth hormone (GH)”, as used herein, is intended to include growth hormone in particular of human origin, as obtained by isolation from biological fluids or as obtained by DNA recombinant techniques from prokaryotic or eukaryotic host cells, as well as its salts, functional derivatives, variants, analogs and active fragments.

GH is a hormone with pleiotropic effects that result from the complex mechanisms regulating its synthesis and secretion as well as from the GH downstream effects resulting in the activation or inhibition of a variety of different intracellular signaling pathways, responsible for different biological effects of GH. At the cellular level, GH binds to one single receptor, but activates multiple responses within individual target cells. GH-responsive genes include IGF-I which is the major mediator of GH action on somatic growth, and also other proteins involved in the regulation of the metabolic effects of GH. Upon administration of exogenous GH, the effects on somatic growth are long-term, but in the short term they can be evaluated by a variety of markers in peripheral blood that reflect the onset of its biological action.

Recombinant human growth hormone can typically be administered to children in a daily dosage ranging from about 0.02 mg/kg/d of body weight up to about 0.07 mg/kg/d of body weight. This dosage may be given daily or accumulated as weekly dose, or the accumulated weekly dose be split into 3 or 6 equal doses per week.

The response to GH treatment, short-term as well as long-term, displays considerable inter individual variability. This is particularly evident for the endpoint of paediatric GH administration, i.e. the growth response, which varies significantly between subjects with TS but is also pronounced between children who are affected by GHD.

This variability can be investigated at two different levels. First, at the level of clinical endpoints related to the assessment of the individual growth response to GH administration and commonly used in the clinical management of short stature subjects. Secondly, at the genotype level, which can be investigated by identifying the genetic factors responsible for the variation of the above clinical endpoints associated to the response to GH intervention.

Growth prediction models attempt to predict the individual response to GH treatment based on either pre-treatment characteristics and/or on response after a short period of GH administration in comparison to the group response. Pre-treatment parameters used in existing prediction models for idiopathic GHD and Turner Syndrome children receiving GH therapy include auxological criteria, indices of endogenous GH secretion, biological markers of GH action such as insulin-like growth factors (IGF) and their binding proteins (IGFBP), and bone turnover markers.

A clear definition of growth response after intervention with GH is lacking and criteria for defining satisfactory GH response targets are yet to be developed (Bakker et al, J Clin. Endo. Metabol., 2008). Increase in height and change in height velocity are useful in clinical practice to assess the

response to GH (GH research society, J Clin Endo Metabol, 2000). Accurate determination of height velocity, continue to be the most important parameters in monitoring the response to treatment (Wetterau & Cohen, Horm Res, 2000), and these changes as compared to relevant population standards, SDS values. rhGH administration is well documented to induce adipose tissue lipolysis (Richelsen B., Horm Res., 1997). It has been shown that adipose tissue mass is significantly reduced in GHD children (Leger et al, J Clin Endo Metabol, 1998). The change in the Body Mass Index, or BMI, a simple anthropometric method to measure changes adiposity, has been shown to be significantly greater in GHD children than in non-GHD (Tillmann et al, Clin Endo, 2000).

The range of GH response is however rather large and these differences can be attributed to various factors including molecular, biochemical and genetic factors. In the scope of the current patent application, a series of candidate genes were examined that were linked to the GH receptor mechanism, to the postreceptor signaling cascade and the robustness of this cascade, to IGF-I or GH transcriptional and translational efficiency and to other candidates linked to the downstream physiological effects of GH administration.

Response to GH treatment is evaluated herein through several quantitative growth related endpoints. These are Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2.

Baseline according to this invention is defined as the patient's clinical and biological characteristics before GH treatment initiation. Year 1 is defined as the patient's clinical and biological characteristics at 1 year after treatment and Year 2 is defined as the patient's clinical and biological characteristics at 2 years after treatment with GH.

In recent years pharmacogenomics—inclusive of pharmacogenetics, as described in the present patent application—(PGx) has come into focus of physicians. Pharmacogenetics can be viewed as the study of inter-individual variations in DNA sequence as related to drug response. In this context the genome of an individual is analyzed leading to the description of genetic markers or susceptibility alterations of significance in this regard.

According to the present invention, the variability of the GH response was assessed by detecting genetic determinants potentially linked with Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2 in GH-treated GHD or TS children (genotyping). This approach is of relevance not only in evaluating the efficacy of response to GH treatment but also the treatment's safety profile and long-term consequences. It has been documented that potential side effects of GH treatment include changes in insulin insensitivity and thus the development of impaired glucose tolerance, which can be monitored and depicted by standard clinical and laboratory measures. Within this context, the identification of the genetic determinants will allow prediction of individual response to GH administration and thus stratify the patients for drug administration.

To understand the genetic factors that underlie heritable diseases or the response to pharmacological treatment, classical genetics examines a single gene or a group of a few genes of interest in relation to the trait associated to the heritable diseases or the response to pharmacological treatment. Genomics, on the other hand, allows performance of this search for genetic determinants that result in particular

phenotypic characteristics at the level of the entire genome. In the present study, the following genomic techniques were used:

Genotyping; through the identification of DNA variations, this method was used to detect genetic determinants in candidate genes that are potentially linked with GHD, TS or different response rates to GH treatment in these two diseases. The search for DNA variants was performed using single nucleotide polymorphisms (SNPs) as genetic markers. A SNP is a DNA locus at which the DNA sequence of two individuals carrying distinct alleles differs by one single nucleotide.

SNPs are the most common human genetic polymorphisms and their density on the genome is very high. Nearly 1.8 million SNPs have been discovered and characterized so far and are publicly available in several major databases (www.hapmap.org, October 2004). Identification of the SNPs of interest according to this invention can be performed with a method developed by Affymetrix or a comparable technique (Matsuzaki H et al., *Genome Research* 2004; 14:414-425). An association between a genetic marker (or a set of genetic markers called a haplotype) and a disease or response to treatment (the phenotype) indicates that a disease- or response-susceptibility gene may lie in the vicinity of the marker. This association is detected as a statistically significant difference in the frequency of a particular allele or genotype at an SNP locus (or the difference in frequency of a haplotypes over several contiguous SNP loci) between patient groups with different phenotypes. This association can be detected either considering the heterozygote and homozygote status of the alleles for a given SNP, the so-called genotypic association, or on the basis of the presence of one or the other of the allele for a given SNP, the so-called allelic association. These association analyses are carried out using non parametric statistical methods, the Krustal-Wallis test for genotypic and the Mann Whitney test for allelic association with a quantitative variable.

Once a SNP has been found to be associated to a disease or response to treatment, categorical predictive analysis is required to further determine which allele is best associated to the response to treatment, and thus could serve as a predictive marker. This categorical analysis is carried out with Fisher exact test to examine the significance of the association between two variables, the response (low or high) and the genotype, in a 2x2 contingency table.

Moreover, predictive genetic markers are selected based on a Fisher p-value, corrected for multiple testing, that is less than or equal to 5% and a positive predictive value threshold greater than or equal to 40% or a negative predictive value threshold greater than or equal to 90%. Alternative genotype frequencies in the study population must be greater than or equal to 15 and less than or equal to 85%.

Relative Risks together with the associated confidence interval indicated in brackets are reported as well as the predictive positive values.

The effects of the combined diplotypes for combinations of 2 individual genetic markers were also considered. This is equivalent of the "and" term of Boolean logic.

Complementary categorical analyses can be performed for significant markers, considering the overall population, defined by three groups: Low responders, High responders, and Intermediate group (being neither Low nor High).

The terms "trait" and "phenotype" may be used interchangeably and refer to any clinically distinguishable, detectable or otherwise measurable property of an organism such as symptoms of, or susceptibility to a disease for example. Typically the terms "trait" or "phenotype" are used to refer to

symptoms of, or susceptibility to GHD or TS; or to refer to an individual's response to a drug acting against GHD or TS.

As used herein, the term "allele" refers to one of the variant forms of a biallelic or multiallelic alteration, differing from other forms in its nucleotide sequence. Typically the most frequent identified allele is designated as the major allele whereas the other allele(s) are designated as minor allele(s). Diploid organisms may be homozygous or heterozygous for an allelic form.

The term "polymorphism" as used herein refers to the occurrence of two or more alternative genomic sequences or alleles between or among different genomes or individuals. "Polymorphic" refers to the condition in which two or more variants of a specific genomic sequence can be found in a population. A "polymorphic site" is the locus at which the variation occurs. A polymorphism may comprise a substitution, deletion or insertion of one or more nucleotides. A SNP is a single base pair change. Typically a single nucleotide polymorphism is the replacement of one nucleotide by another nucleotide at the polymorphic site.

As will be discussed below in more details, the alteration ("susceptibility alteration") in a gene or polypeptide according to the invention may be any nucleotide or amino acid alteration associated to the response to growth hormone (GH) treatment in GHD or TS children.

A genotypic marker is defined by an association between response and a genotype or pair of genotypes. These can be the dominance test (carrier of major allele, homozygous and heterozygous, vs. non-carrier of major allele, homozygous minor allele) or the recessive test, (carrier of minor allele, homozygous and heterozygous, vs. non carrier of minor allele, homozygous major allele).

Candidate markers are assessed for their significance in both continuous genetic analyses and categorical analyses in the whole study population separated in a GHD population and a TS population.

A trait associated polymorphism may be any form of mutation(s), deletion(s), rearrangement(s) and/or insertion(s) in the coding and/or non-coding region of the gene, either isolated or in various combination(s). Mutations more specifically include point mutations. Deletions may encompass any region of one or more residues in a coding or non-coding portion of the gene. Typical deletions affect small regions, such as domains (introns) or repeated sequences or fragments of less than about 50 consecutive base pairs, although larger deletions may occur as well. Insertions may encompass the addition of one or several residues in a coding or non-coding portion of the gene. Insertions may typically comprise an addition of between 1 and 50 base pairs in the gene. Rearrangements include for instance sequence inversions. An alteration may also be an aberrant modification of the polynucleotide sequence, and may be silent (i.e., create no modification in the amino acid sequence of the protein), or may result, for instance, in amino acid substitutions, frameshift mutations, stop codons, RNA splicing, e.g. the presence of a non-wild type splicing pattern of a messenger RNA transcript, or RNA or protein instability or a non-wild type level of the polypeptide. Also, the alteration may result in the production of a polypeptide with altered function or stability, or cause a reduction or increase in protein expression levels.

Typical susceptibility alterations or genetic markers are SNPs as described above.

The presence of an alteration in a gene may be detected by any technique known per se to the skilled artisan, including sequencing, pyrosequencing, selective hybridisation, selective amplification and/or mass spectrometry including matrix-assisted laser desorption/ionization time-of-flight

mass spectrometry (MALDI-TOF MS). In a particular embodiment, the alteration is detected by selective nucleic acid amplification using one or several specific primers. The alteration is detected by selective hybridization using one or several specific probes.

Further techniques include gel electrophoresis-based genotyping methods such as PCR coupled with restriction fragment length polymorphism (RFLP) analysis, multiplex PCR, oligonucleotide ligation assay, and minisequencing; fluorescent dye-based genotyping technologies such as oligonucleotide ligation assay, pyrosequencing, single-base extension with fluorescence detection, homogeneous solution hybridization such as TaqMan, and molecular beacon genotyping; rolling circle amplification and Invader assays as well as DNA chip-based microarray and mass spectrometry genotyping technologies.

Protein expression analysis methods are known in the art and include 2-dimensional gel-electrophoresis, mass spectrometry and antibody microarrays.

Sequencing can be carried out using techniques well known in the art, e.g. using automatic sequencers. The sequencing may be performed on the complete gene or, more preferably, on specific domains thereof, typically those known or suspected to carry deleterious mutations or other alterations.

Amplification may be performed according to various techniques known in the art, such as by polymerase chain reaction (PCR), ligase chain reaction (LCR) and strand displacement amplification (SDA). These techniques can be performed using commercially available reagents and protocols. A preferred technique is allele-specific PCR.

The term "gene" as used herein shall be construed to include any type of coding nucleic acid region, including genomic DNA (gDNA), complementary DNA (cDNA), synthetic or semi-synthetic DNA, any form of corresponding RNA (e.g., mRNA), etc., as well as non coding sequences, such as introns, 5'- or 3'-untranslated sequences or regulatory sequences (e.g., promoter or enhancer), etc. The term gene particularly includes recombinant nucleic acids, i.e., any non naturally occurring nucleic acid molecule created artificially, e.g., by assembling, cutting, ligating or amplifying sequences. A gene is typically double-stranded, although other forms may be contemplated, such as single-stranded. Genes may be obtained from various sources and according to various techniques known in the art, such as by screening DNA libraries or by amplification from various natural sources. Recombinant nucleic acids may be prepared by conventional techniques, including chemical synthesis, genetic engineering, enzymatic techniques, or a combination thereof. The term "gene" may comprise any and all splicing variants of said gene.

The term "polypeptide" designates, within the context of this invention, a polymer of amino acids without regard to the length of the polymer; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. A fragment of a polypeptide designates any portion of at least 8 consecutive amino acids of a sequence of said protein, preferably of at least about 15, more preferably of at least about 20, further preferably of at least 50, 100, 250, 300 or 350 amino acids. This term also includes post-translational or post-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides variants which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino

acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian systems etc.), polypeptides with substituted linkages, as well as other modifications known in the art, both naturally occurring and non-naturally occurring.

The term "treat" or "treating" as used herein is meant to ameliorate, alleviate symptoms, eliminate the causation of the symptoms either on a temporary or permanent basis, or to prevent or slow the appearance of symptoms of the named disorder or condition. The term "treatment" as used herein also encompasses the term "prevention of the disorder", which is, e.g., manifested by delaying the onset of the symptoms of the disorder to a medically significant extent. Treatment of the disorder is, e.g., manifested by a decrease in the symptoms associated with the disorder or an amelioration of the reoccurrence of the symptoms of the disorder.

"Response" to growth hormone treatment in an individual suffering from GHD or TS in the sense of the present invention is understood to be residual disease activity upon a period of approximately one (from year one to year 2) or two (from baseline to year 2) years of growth hormone treatment, with the clinical endpoints annualized. More specifically the residual disease activity is herein associated to Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2.

"High responders" or "good responders" refer to those individuals who can be identified to show improved response to two years of growth hormone treatment in comparison to the GHD or TS population who exhibit an average response level upon two years of growth hormone treatment. The "high response" or "good response" is exhibited by reduced residual disease activity.

"Low responders" or "poor responders" refer to those individuals who can be identified to show impaired response to two years of growth hormone treatment in comparison to the GHD or TS population who exhibit an average response level upon two years of growth hormone treatment.

The present invention stems from the pharmacogenomics analysis evaluating gene variations in a group of 93 GHD and 42 TS patients.

In the specific examples as disclosed in the present patent application, extreme categories required for categorical genetic analyses are defined by quartiles:

the low responders are herein represented by the first and lower quartile (designated as Q1) also designated by the lowest 25% of the data (25th percentile);

the high responders are herein represented by the third quartile and upper quartile (designated as Q3) also designated by the highest 75% (75th percentile);

the intermediate group is herein represented as the data from >Q1 and <Q3 also designated as the intermediary 50% of the data.

These quartiles were defined by taking into consideration the age group of patients.

The present invention is directed in a first embodiment to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in the STAT Gene Cluster rs2293152 the CC genotype is present; and

- b. predicting from the presence of the CC genotype in the STAT Gene Cluster rs2293152 an intermediate or high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PIK3CG rs3173908 either the TT or TC genotype is present; and
- b. predicting from the presence of either the TT or TC genotype in PIK3CG rs3173908 an intermediate or high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PIK3CG rs4730205 the CC genotype is present; and
- b. predicting from the presence of the CC genotype in PIK3CG rs4730205 a low Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PIK3R3 rs7533750 the CC or GC genotype is present; and
- b. predicting from the presence of the CC or GC genotype in PIK3R3 rs7533750 a high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in CDKN1A rs1801270 either the AA or AC genotype is present; and
- b. predicting from the presence of either the AA or AC genotype in CDKN1A rs1801270 a high Change in Height in cm from 1 year to 2 years of treatment.

In another embodiment the present invention is directed to a method of identifying the Change in Height SDS from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in LHX4 rs7536561 the AA genotype is present; and
- b. predicting from the presence of the AA genotype in LHX4 rs7536561 a high Change in Height SDS from 1 year to 2 years of treatment.

In another embodiment the present invention is directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in ADIPOQ rs3821799 the CC genotype is present; and

- b. predicting from the presence of the CC genotype in ADIPOQ rs3821799 an intermediate or low Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in IGF2R rs687088 either the TT or TC genotype is present; and
- b. predicting from the presence of the TT or TC genotype in IGF2R rs687088 a low Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in MYC rs4645956 either the TT or TC genotype is present; and
- b. predicting from the presence of the TT or TC genotype in MYC rs4645956 an intermediate or high Change in Height in cm from 1 year to 2 years of treatment.

In another embodiment the present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in INPPL1 rs2276048 either the GG or AG genotype is present; and
- b. predicting from the presence of the GG or AG genotype in INPPL1 rs2276048 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in SOS1 rs2888586 the CC genotype is present; and
- b. predicting from the presence of the CC genotype in SOS1 rs2888586 an intermediate or low Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in SOS1 rs2168043 either the AA or AC genotype is present; and
- b. predicting from the presence of either the AA or AC genotype in SOS1 rs2168043 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in CCND2 rs3217862 either the GG or TG genotype is present; and

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- b. predicting from the presence of the GG or TG genotype in CCND2 rs3217862 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in GAB1 rs3805236 the GG genotype is present; and
- b. predicting from the presence of the GG genotype in GAB1 rs3805236 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PPARGC1A rs7677000 either the TT or TC genotype is present; and
- b. predicting from the presence of either the TT or TC genotype in PPARGC1A rs7677000 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height SDS from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in ID1 rs6058189 either the GG or AG genotype is present; and
- b. predicting from the presence of either the GG or AG genotype in ID1 rs6058189 an intermediate or low Change in Height SDS from 1 year to 2 years of treatment.

The present invention is directed to a method of identifying the Change in Height SDS from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PPP1CC rs7960552 the TT genotype is present; and
- b. predicting from the presence of the TT genotype in PPP1CC rs7960552 a low Change in Height SDS from 1 year to 2 years of treatment.

The present invention is directed to a method of identifying the Change in Height SDS from 1 year to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in ESR1 rs827423 the AA genotype is present; and
- b. predicting from the presence of the AA genotype in ESR1 rs827423 a high Change in Height SDS from 1 year to 2 years of treatment.

In another embodiment the present invention is directed to a method of identifying the Change in Height SDS from Baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in CYR61 rs9658584 either the CC or CG genotype is present; and
- b. predicting from the presence of the CC or CG genotype in CYR61 rs9658584 a low Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height SDS from Baseline to 2 years of

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treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in SH2B2 rs2960266 the CC genotype is present; and
- b. predicting from the presence of the CC genotype in SH2B2 rs2960266 a high Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height SDS from Baseline to 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PPARGC1A rs7677000 either the TT or TC genotype is present; and
- b. predicting from the presence of either the TT or TC genotype in rs7677000 a high Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in CYR61 rs9658584 either the CC or CG genotype is present; and
- b. predicting from the presence of either the CC or CG genotype in CYR61 rs9658584 a low Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in INS rs3842748 either the CC or CG genotype is present; and
- b. predicting from the presence of either the CC or CG genotype in INS rs3842748 an intermediate or low Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PDK1 rs12693005 either the CC or TC genotype is present; and
- b. predicting from the presence of either the CC or TC genotype in PDK1 rs12693005 a high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in SOS1 rs2168043 either the AA or AC genotype is present; and
- b. predicting from the presence of either the AA or AC genotype in SOS1 rs2168043 a high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PPP1CB rs6547874 the GG genotype is present; and

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- b. predicting from the presence of the GG genotype in PPP1CB rs6547874 an intermediate or high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PPP1CB rs6706858 the GG genotype is present; and
- b. predicting from the presence of the GG genotype in PPP1CB rs6706858 an intermediate or high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Growth Hormone Deficiency, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PPP1CB rs3190 the GG genotype is present; and
- b. predicting from the presence of the GG genotype in PPP1CB rs3190 an intermediate or high Height Velocity SDS at 2 years of treatment.

In another embodiment the present invention is directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in GATA1 rs5906709 the G allele (either G₊, GG or AG) genotype is present; and
- b. predicting from the presence of the G allele (either G₊, GG or AG) genotype in GATA1 rs5906709 a high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in IGFALS rs3817899 either the CC or CG genotype is present; and
- b. predicting from the presence of either the CC or CG genotype in IGFALS rs3817899 a high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in SOS1 rs2278914 either the GG or AG genotype is present; and
- b. predicting from the presence of either the GG or AG genotype in SOS1 rs2278914 a high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PTPN1 rs3787335 either the GG or TG genotype is present; and
- b. predicting from the presence of either the GG or TG genotype in PTPN1 rs3787335 a low Change in Height in cm from 1 year to 2 years of treatment.

In another embodiment the present invention is directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

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- a. determining in a DNA sample of the individual whether in SLC2A1 rs751210 either the AA or AG genotype is present; and

- b. predicting from the presence of either the AA or AG genotype in SLC2A1 rs751210 a high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual the genotype of PPARG rs1151996; and
- b1. predicting from the presence of the CC or CA genotype in PPARG rs1151996 a low Change in Height in cm from 1 year to 2 years of treatment; or
- b2. predicting from the presence of the AA genotype in PPARG rs1151996 an intermediate or high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual the genotype of PPARG rs709149; and
- b1. predicting from the presence of the AA or AG genotype in PPARG rs709149 a low Change in Height in cm from 1 year to 2 years of treatment; or
- b2. predicting from the presence of the GG genotype in PPARG rs709149 an intermediate or high Change in Height in cm from 1 year to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from 1 year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual the genotype of PPARG rs1175540; and
- b1. predicting from the presence of the AA or AC genotype in PPARG rs1175540 a low Change in Height in cm from 1 year to 2 years of treatment; or
- b2. predicting from the presence of the CC genotype in PPARG rs1175540 an intermediate or high Change in Height in cm from 1 year to 2 years of treatment.

In another embodiment the present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PTPN1 rs3787335 either the GG or TG genotype is present; and
- b. predicting from the presence of either the GG or TG genotype in PTPN1 rs3787335 a low Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in JAK2 rs2149556 the TT genotype is present; and
- b. predicting from the presence of the TT genotype in JAK2 rs2149556 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

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- a. determining in a DNA sample of the individual whether in JAK2 rs7034753 the GG genotype is present; and
- b. predicting from the presence of either the GG genotype in JAK2 rs7034753 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in JAK2 rs7046736 either the AA or AC or CC genotype is present; and
- b1. predicting from the presence of either the AA or AC genotype in JAK2 rs7046736 a high Change in Height in cm from baseline to 2 years of treatment, or
- b2. predicting from the presence of the CC genotype in JAK2 rs7046736 an intermediate or low Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in JAK2 rs7043371 the AA genotype is present; and
- b. predicting from the presence of the AA genotype in JAK2 rs7043371 a high Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in SLC2A1 rs751210 either the AA or AG or GG genotype is present; and
- b1. predicting from the presence of either the AA or AG genotype in SLC2A1 rs751210 a high Change in Height in cm from baseline to 2 years of treatment, or
- b2. predicting from the presence of either the GG genotype in SLC2A1 rs751210 an intermediate or low Change in Height in cm from baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height in cm from baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PIK3CG rs4460309 either the CC, TT or TC genotype is present; and
- b1. predicting from the presence of either TT or TC genotype in PIK3CG rs4460309 an intermediate or low Change in Height in cm from baseline to 2 years of treatment, or
- b2. predicting from the presence of the CC genotype in PIK3CG rs4460309 a high change in Height in cm from baseline to 2 years of treatment.

In another embodiment the present invention is directed to a method of identifying the Change in Height SDS from 1 year to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in GATA1 rs5906709 the G allele (G-, GG or AG) is present; and
- b. predicting from the presence of the G allele (G, GG or AG) in GATA1 rs5906709 a high Change in Height SDS from 1 year to 2 years of treatment.

The present invention is directed to a method of identifying the Change in Height SDS from 1 year to 2 years of treatment

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with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in IGFALS rs3817899 either the CC or CG genotype is present; and
- b. predicting from the presence of either the CC or CG genotype in IGFALS rs3817899 an intermediate or high Change in Height SDS from 1 year to 2 years of treatment.

In another embodiment the present invention is directed to a method of identifying the Change in Height SDS from Baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PTPN1 rs3787335 either the GG or TG or TT genotype is present; and
- b1. predicting from the presence of either the GG or TG genotype in PTPN1 rs3787335 a low Change in Height SDS from Baseline to 2 years of treatment, or
- b2. predicting from the presence of either the TT genotype in PTPN1 rs3787335 an intermediate or high Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height SDS from Baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual the genotype of PTPN1 rs13041704 whether the CC or AC or AA genotype is present; and
- b1. predicting from the presence of the CC or AC genotype in PTPN1 rs13041704 a low Change in Height SDS from Baseline to 2 years of treatment; or
- b2. predicting from the presence of the AA genotype in PTPN1 rs13041704 an intermediate or high Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height SDS from Baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in CDK4 rs2069502 the TT, TC or CC genotype is present; and
- b1. predicting from the presence of the CC genotype in CDK4 rs2069502 an intermediate or high Change in Height SDS from Baseline to 2 years of treatment; or b2. predicting from the presence of the TT or TC genotype in CDK4 rs2069502 a low Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height SDS from Baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in IRS2 rs7981705 either TT or TC genotype is present; and
- b. predicting from the presence of either the TT or TC genotype in IRS2 rs7981705 a low Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Change in Height SDS from Baseline to 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

- a. determining in a DNA sample of the individual whether in PIK3CG rs4460309 either the CC, TT or TC genotype is present; and

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b1. predicting from the presence of either the TT or TC genotype in PIK3CG rs4460309 an intermediate or low Change in Height SDS from Baseline to 2 years of treatment, or

b2. predicting from the presence of the CC genotype in PIK3CG rs4460309 a high Change in Height SDS from Baseline to 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual the genotype of in LEPR rs4655537; and

b1. predicting from the presence of the AA or AG genotype in LEPR rs4655537 a low Height Velocity SDS at 2 years of treatment; or

b2. predicting from the presence of the GG genotype in LEPR rs4655537 an intermediate or high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in SREBF1 rs9899634 the TT genotype is present; and

b. predicting from the presence of the TT genotype in SREBF1 rs9899634 a high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in GATA1 rs5906709 the G allele (G-, GG or GA) is present; and

b. predicting from the presence of the G allele (G-, GG or GA) in GATA1 rs5906709 a high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in INPPL1 rs2276048 either the GG or AG genotype is present; and

b. predicting from the presence of either the GG or AG genotype in INPPL1 rs2276048 a high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual the genotype of in PTPN1 rs13041704; and

b1. predicting from the presence of the CC or AC genotype in PTPN1 rs13041704 a low Height Velocity SDS at 2 years of treatment; or

b2. predicting from the presence of the AA genotype in PTPN1 rs13041704 an intermediate or high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in IL6 rs2069840 either the GG or GC genotype is present; and

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b. predicting from the presence of either the GG or GC genotype in IL6 rs2069840 a high Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in CDK2 rs2069408 the AA, GG or AG genotype is present; and

b1. predicting from the presence of the AA genotype in CDK2 rs2069408 an intermediate or low Height Velocity SDS at 2 years of treatment; or

b2. predicting from the presence of the GG or AG genotype in CDK2 rs2069408 a high Height Velocity SDS at 2 years of treatment

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in RB1 rs4151551 either the TT or TG genotype is present; and

b. predicting from the presence of either the TT or TG genotype in RB1 rs4151551 an intermediate or low Height Velocity SDS at 2 years of treatment.

The present invention is also directed to a method of identifying the Height Velocity SDS at 2 years of treatment with growth hormone in an individual having Turner Syndrome, the method comprising the steps of:

a. determining in a DNA sample of the individual whether in AKT2 rs4802071 the TT genotype is present; and

b. predicting from the presence of the TT genotype in AKT2 rs4802071 a high Height Velocity SDS at 2 years of treatment.

In all the above sections, A, T, C and G represent adenine, thymine, cytosine and guanine, respectively.

DNA samples according to the present invention may be obtained by taking blood samples from an individual.

Preferably, the treatment with growth hormone has been carried out during about 2 years. In a further embodiment the present invention is directed to a kit for detecting a genetic markers or a combination of genetic markers that are associated with the level of response to treatment with growth hormone, as previously stated in association to biomarker response to GH treatment and in this particular case to IGF-I response.

The kit comprises a probe or a set of oligonucleotide primers designed for identifying each of the alleles in any of the above described genetic variants

Probes and primers that can be used according to the invention preferably are fragments of sequences or hybridize to the sequences shown to be associated with Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2 in response to two years of GH treatment.

The results according to this invention may be applied in approaches of personalized medicine. Personalized medicine is, according to the present patent application, the use of information and data from a patient's genotype to stratify disease, select a medication, provide a therapy, or initiate a preventative measure that is particularly suited to that patient at the time of administration. In addition to genetic information, other factors, including imaging, laboratory, and clinical information about the disease process or the patient play an

equally important role. It is believed that personalized medicine will make it possible in the future to give the appropriate drug, at the appropriate dose, to the appropriate patient, at the appropriate time.

Since the data generated by the present study documents a correlation between growth response to human Growth Hormone (hGH) treatment and the presence of specific genetic variants carried by human patients, the present invention aims at covering body growth resulting of cellular, tissular or somatic growth in human patients modulated or regulated (up or down regulated) by hGH treatment through this variant; in addition the invention aims at covering the use for treatment (and or even diagnostic) purpose of either natural hGH, recombinant hGH, hGH analogs (agonists or antagonists, natural or non natural regardless of their mode of production) acting through this specific genetic variant to modulate growth response in human patients.

Patients with a genotype predictive of a high response can be given the standard dose of GH, i.e. the dose currently used in clinical practice, which is for children a daily dosage ranging from about 0.02 mg/kg of body weight up to about 0.07 mg/kg of body weight.

Alternatively these patients can be given an optimized dose. Patients with markers predictive of a low response would be given an optimized dose of GH or an analog thereof. An optimized dose of GH to be given to a low responder may be an increased dose of GH compared to the standard dose as a dose-response relationship in terms of height velocity in the first 2 years of treatment has been demonstrated; and this in a dose range compatible with the fixed dose used to treat GHD or TS patients in the current settings. Low responders can also be candidate patients for therapies with long acting analogs of GH with a frequency of administration which is decreased.

In a further embodiment the present invention is thus directed to a method for treating Growth Hormone Deficiency (GHD) or Turner Syndrome (TS) in an individual in need thereof, the method comprising the steps of

- identifying the level of response to treatment with growth hormone according to any of the methods described above,
- treating the individual with growth hormone.

In a preferred embodiment, the individual is identified as low responder and is treated with a dose of growth hormone that is optimized compared to the standard dose.

In one embodiment, a low responder is treated with a dose of growth hormone that is increased compared to the standard dose or he is treated with a long-acting analog of growth hormone.

Genetic markers were identified herein as being associated to low or high response, the response herein described being the Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2 after two years of GH treatment. These genetic markers can be considered either alone or in combination in the methods according to the invention.

In a further embodiment, the invention relates to the use of growth hormone in the preparation of a medicament for treating paediatric Growth Hormone Deficiency (GHD) or Turner Syndrome (TS) in an individual in need thereof, wherein the individual has been identified according to any of the methods described above to be a low responder or a high responder to the treatment with growth hormone.

In a further embodiment, the present invention relates also to growth hormone for use in treating paediatric Growth Hormone Deficiency (GHD) or Turner Syndrome (TS) in an

individual in need thereof, wherein the individual has been identified according to any of the methods described above to be a low responder or a high responder to the treatment with growth hormone.

In the method of identifying, kit or method of treating according to the invention the growth hormone is preferably human growth hormone and more preferably recombinant human growth hormone. Particular embodiments of the invention refer to growth hormone as sold under the trade-name SAIZEN®.

Formulations useful in a method of treating a GHD or TS patient according to the invention may be a liquid pharmaceutical formulation comprising growth hormone or a reconstituted freeze-dried formulation comprising growth hormone. Preferably the formulation is stabilized by a polyol, more preferably a disaccharide and even more preferably sucrose.

In the following the present invention shall be illustrated by means of the following examples that are not to be construed as limiting the scope of the invention.

EXAMPLES

Example 1

Genotyping

1.1. Background

GHD and TS and the different auxological responses to GH treatment in the two diseases may each be associated with a specific genetic variation in one or several genes. In the present study, the search for associations between genes containing variations, in the present invention SNPs, so-called susceptibility genes, and disease or response to treatment was focused on candidate genes that were selected based on the physiological role of the proteins they encode and their potential implication in the diseases, GHD and TS, or in the response to GH treatment. The list of selected candidate genes is given in Table 1.

Response to GH treatment was measured by Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2 in response to two years of treatment with GH.

TABLE 1

GHD OR TS RELATED GENES	
FGF-R3	GH-1
GH-R	GHRH
GHRH-R	Glut4
HESX-1	IGF-1
Insulin-VNTR LHX3	LHX4
POU1F1 (Pit-1)	Prop-1
SHOX-1	SHOX-2
STAT-5	
GH & IGF-1 RELATED GENES	
ALS	APS (SH2B2)
β Arrestin-1 (ARRB1)	GAB-1
GH1	GH-R
GHRH	GHRH-R
ID1 & ID2	IGF-I
IGF-I-R	IGF-II
IGF-II-R	IGF-BP3
IGF-BP1	IGF-BP-2
IGF-BP10	JAK2
MAP Kinase	PGDF-R β

TABLE 1-continued

PTP1 β (PTPN1)	PI3Kinase subunits
p60dok	SHC1
STAT-5	SOCS-2
STAT-3	GRB10
SHPS-1	SH2B2
INSULIN RELATED GENES	
Adiponectin (Acrp30 or AdipoQ)	ADRB3)
AKT 1 & AKT 2	Glut4
Glut1 also known as SLCA1	GRB2
Insulin (VNTR)	Insulin-R
IRS-1	IRS-2
IRS-4	LEP (leptin)
LEP-R (Leptin-R) (Ob-R)	pp120/HA4 (CEACAM8)
PI3Kinase p85	PI3Kinase p110 α and p110 β (polymorphic GATA binding site)
	Protein-Phosphatase 1 (PP1)
PTP1 β	PDK1
PPAR γ	PPAR γ Co-activator1 (PGC1)
RAs	SHIP2
SHC1	SOS 1 & 2
SREBP-1c	TNF α
BONE METABOLISM RELATED GENES	
AR	Aromatase
ER- α	GPCRs
Myogenin	MyoD
p21	PKC α
RA-R	
ONCOGENES & INFLAMMATORY RELATED GENES	
bcl-2	c-Erb B1
c-fos	c-jun
jun-b	c-myc
CDK2 CDK4 and CDK6	Cyclin D
TGF- α	TGF- β
p53	Ras
Rb	WT1
INFLAMMATION RELATED GENES	
GATA1	IL-4
IL-6	TNF- α

The candidate genes selected have been previously implicated in growth, the mechanism of action of growth hormone, or in growth hormone deficiency or Turner syndrome. The purpose of the study was to investigate whether TS, GHD in association to Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2 in response to two years of GH treatment in these diseases is correlated with a specific DNA variant or pattern of variants. The existence of such a correlation would indicate that either the gene(s) carrying the identified variant(s) or one or more genes lying in the vicinity of the variants may be (a) susceptibility gene(s).

1.2. Materials and Methods

1.2.1. DNA Samples Extraction and Preparation

The analysis was performed on DNA extracted from polymorphonuclear leucocytes. A total of 319 blood samples were received. Out of these 319, 3 samples were not double coded and were destroyed by the genomic laboratory. The 316 samples remaining went into the genomic analysis. Out of these 316 DNA samples analysed, 3 were duplicates resulting in 313 DNAs analysed corresponding to 313 patients in the Predict study. Upon transfer of the clinical data, 3 patients with DNA analysed did not have any clinical data collected.

Thus 310 patients were genotyped and eligible for the association studies.

Regarding the year two analysis of the follow-up study, 310 patients were genotyped and eligible for the association studies. Only 150 (all Tanner Stages) consented to participate to

the two year study after the one year follow-up study. 49 TS and 101 GHD have the baseline, the year two auxological values required for the association described in the present patent application. Only Tanner Stage 1 & 2 were considered (93 GHD children and 42 TS girls) for the genetic analysis in the present patent application.

DNA was extracted from 316 blood samples between November 2006 and November 2007 using a Qiagen kit (QIAamp DNA Blood Midi Kit/Lot 127140243/Ref 51185). After extraction DNA quality and quantity were controlled (QC.1 and QC.2) by measures of absorbance at wavelengths of 260 nm and 280 nm using a (Molecular Devices Spectra-max Plus) spectrophotometer and electrophoresis of DNA samples on agarose gels.

QC.1: 260 nm/280 nm absorbance ratio and DNA concentration calculated from the 280 nm absorbance value.

QC.2: Electrophoresis on agarose gel.

All 316 DNA samples passed the acceptance criteria defined for QC.1: absorbance ratio between 1.7 and 2.1 and DNA concentration above 50 ng/ μ L.

All 316 DNA samples passed the acceptance criteria defined for QC.2: for each sample, one clearly defined band visible on agarose gel after electrophoresis at a high molecular weight corresponding to non-degraded genomic DNA.

An aliquot of 3 μ g of DNA from each sample was distributed into four 96 well micro-plates. Each micro-plate also contained a negative control and a reference genomic DNA (referred to as DNA 103).

The four micro-plates were assigned a name ranging from Saizen-PL1 to Saizen-PL4. The 316 samples were assigned a genotyping number ranging from 50-1657 to 50-1972.

1.2.2. DNA Microarray Technology

DNA microarray technology was used for genotyping. A microarray is an experimental tool that was developed to meet the needs of whole genome analysis to simultaneously screen a vast number of genes or gene products. Due to its miniaturised format and amenability to automation, a microarray is suitable for high-throughput analysis. The technique is based on the ability of two nucleic acid molecules to selectively bind (hybridise) to one another if their sequences are complementary. A set of different nucleic acid fragments, the probe, is covalently attached at defined positions on a solid support of a few square centimeters. The genetic material to be analysed, the target, is exposed to the arrayed probe. Using the selective hybridisation property of nucleic acids, the probes are designed in such a way that they will bind only to those target molecules that are of interest in the particular investigation. Selective labelling of the bound complex and the knowledge of the identity of each probe based on its location on the array allows the identification of the target molecule.

In this experiment, the Illumina GoldenGate technology protocol was used. This technology is based on 3 micron silica beads that self assemble in micro-wells on either two substrates, fiber optic bundles or planar silica slides. When randomly assembled on one of these two substrates, the beads had a uniform spacing of \sim 5.7 microns. Each bead is covered with hundreds of thousands of copies of a specific oligonucleotide that act as capture sequences.

1536 SNPs were selected from 103 candidate genes and 1448 SNPs were successfully genotyped for all individuals and analysed in 97 candidate genes out of these 1448 SNPs.

The samples were randomly distributed by the biobanking technician on four 96-well microplate. Each microplate was then processed sequentially using a different Illumina kit and Sentrix Array Matrix for each plate.

1.2.3. Genetics Analysis

For continuous quantitative data, The R version 2.9.0 software (R: A language and environment for statistical computing) was used for data analysis to perform quantitative association analysis. The “kruskal.test” function was used to perform non-parametric Kruskal-Wallis sign rank test of single marker.

For Categorical analyses, association analysis software algorithms for single marker association analysis, for sex chromosome linked copy number association analyses, for haplotype association analyses and for analysis of all two marker diplotype combinations were used.

Only the available data was integrated in the analysis, no imputation was carried out.

1.2.4. Estimation of Linkage Disequilibrium (LD) Structure

The number of Linkage Disequilibrium (LD) blocks in each gene was estimated in the two disease groups by means of the “ALLELE” SAS procedure, through the JMP Genomics interface. This was used to compute adjusted p-values.

1.2.5. Statistical Testing

Continuous Analyses

For a given phenotype at year two (Change in Height in cm from Baseline to Year 2, Change in Height in cm from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, and Height Velocity SDS at Year 2), new variables were built, indicating major and minor allele presence.

Genotypic Association

The association between the genotype and the phenotypic quantitative variable was evaluated by the Kruskal-Wallis association test implemented by the ‘kruskal.test’ function of the R software package. The main output of this procedure was a table essentially giving the probability levels (p-values) for the genotype categorical effect on phenotype, for each SNP and disease group.

Allelic Association

Similarly, the association between the presence of the major allele and the biomarker quantitative variable was also evaluated by the Kruskal-Wallis association test implemented by the ‘kruskal.test’ function of the R software package. The same was repeated for the minor allele.

The output of these procedures was a table essentially giving the p-values for the effect on phenotype of the presence of the corresponding allele, for each SNP and disease group. Selection of Significantly Associated SNPs and Genes

A summary table was produced to join output of the association tests performed (p-value and nature of the corresponding genetic variable) together with disease type, SNP and gene names, number of SNPs tested and of LD blocks in the gene, and SNP minor allele frequency (MAF) and call rate.

For selection of significant associations, Bonferroni correction for multiple testing was applied to compute adjusted p-values based on the number of tested LD blocks in the same gene (Table 5; nominal p-value).

An initial aggressive selection of genes containing SNPs eligible for association was performed by selecting observations where the MAF was greater than 0.1, so as to have a frequency of the minor allele frequency (MAF) above 10% (Table 5; MAF), the call rate greater than 0.95 (Table 5; call rate), and the initial, unadjusted p-value was lower than the nominal 0.05 significance cut-off.

The final selection of significantly associated genes was based on adjustment of the nominal marker p-values by the number of LD-blocks (Table 5; adjusted p-values), used as an estimate of the number of independent tests applied to each gene.

Relevant Information:

R version: 2.9.0

R citation:

R Development Core Team (2009). R: A language and environment for

statistical computing. R Foundation for Statistical Computing,

Vienna, Austria. ISBN 3-900051-07-0, URL <http://www.R-project.org>.

Categorical Analysis: Prediction

A selection of SNPs were assessed for potential use in patient stratification and association with the following auxological endpoint parameters at year two: Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2.

These qualitative continuous variables were classified into categories which were analyzed as 2x2 contingency tables using Fisher’s exact test for the chi-square statistic.

High responders were defined as having values for each of the four endpoint variables that were greater than or equal to the 3rd quartile of the distribution for each variable.

Low responders, were defined as having values for each of the 4 endpoint variables that were less than or equal to the 1st quartile of the distribution for each variable.

Intermediate responders were defined as having values for each of the 4 endpoint variables that were less than Q3 and greater than Q1.

Quartiles were calculated independently for each of 3 age groups within each of the endpoint variables. The upper (3rd) and lower (1st) Quartile values are given in Table 2 below.

Quartiles were defined by taking into consideration the age group as well.

TABLE 2

		Quartile Thresholds for Different Age Groups within Five Auxological two year endpoints for GHD and TS children.									
			GHD								
			AUHTC02	Age < 8	14.67	18.96	7	7	14	28	
				8 <= Age <= 12	13.11	16.88	13	13	26	52	
				Age > 12	14.2	17.46	4	4	5	13	
		AUHTC12	Age < 8	6.27	8.23	7	8	13	28		
			8 <= Age <= 12	5.81	8.08	13	13	26	52		
			Age > 12	6.81	9.65	4	4	5	13		
		AUHSDC02	Age < 8	0.87	1.84	7	7	14	28		
			8 <= Age <= 12	0.44	1.09	14	13	25	52		
			Age > 12	0.29	0.75	4	4	5	13		
		AUHSDC12	Age < 8	0.24	0.56	7	7	14	28		
			8 <= Age <= 12	0	0.36	14	13	25	52		
			Age > 12	-0.1	0.49	4	4	5	13		
		AUHVSDS2	Age < 8	1.07	3.35	7	7	14	28		
			8 <= Age <= 12	-0.26	1.63	13	13	26	52		
			Age > 12	0.57	2	4	4	5	13		
		TS AUHTC02	Age < 8	13.94	15.96	5	5	8	18		
			8 <= Age <= 12	12.48	15.93	5	5	10	20		
			Age > 12	9.7	10.57	1	1	2	4		
		AUHTC12	Age < 8	5.88	7.1	5	5	8	18		
			8 <= Age <= 12	5.1	7.02	5	5	10	20		
			Age > 12	4.39	5.28	1	1	2	4		
		AUHSDC02	Age < 8	0.78	1.27	5	5	8	18		
			8 <= Age <= 12	0.03	0.92	5	5	10	20		
			Age > 12	0.28	0.69	1	1	2	4		
		AUHSDC12	Age < 8	0.09	0.35	5	5	8	18		
			8 <= Age <= 12	-0.13	0.23	6	5	9	20		
			Age > 12	0.35	0.53	1	1	2	4		
		AUHVSDS2	Age < 8	0.09	1.66	5	5	8	18		
			8 <= Age <= 12	-0.29	0.42	5	5	10	20		
			Age > 12	1.86	3.9	1	1	2	4		

Analyses consisted of tests for each of two alternative comparisons, high responders ($\geq Q3$) versus intermediate and low responders ($< Q3$); and low responders ($\leq Q1$) versus intermediate and high responders ($> Q1$). Each of the two contrasts was tested using two distinct genetic models, dominance of major allele (Ma) and recessive for major allele. The major allele (Ma) is defined as the more frequent of the two alternative alleles of each DNA marker and the minor allele (Mi) is defined as the less frequent of the two alternative alleles. The two genotype markers for the dominance major allele test are MaMa or MaMi genotypes versus MiMi genotype. The two genotype markers within the recessive major allele test are MaMa versus MiMi or MaMi genotypes. Each of the two alternative genotype markers is associated (more frequent) in one of the two alternative categories for each contrast. Therefore, each genotype marker of the DNA marker is indicative of one of the two alternative categories.

DNA markers were selected as potential biomarkers if they were associated with one of the five endpoint variables at an adjusted (for multiple tests) Fisher exact p-value that was less than or equal to 0.10. In addition to p-value for the tests, the following parameters of the association were also noted:

Relative risk (RR) and the 95% confidence interval for RR:

RR is the increase in probability of being a category 1 individual (high or low responder, depending on the contrast tested), given that the individual carries the category 1 associated genotype marker relative to the probability of being a category 1 individual given that the individual carries the alternative genotype marker.

Positive predictive value (PPV): the probability of being a category 1 individual (high or low responder depending upon the specific contrast being tested) given that the individual carries the category 1 associated genotype marker. The expected value for PPV given no effect is 25%. Increased departures from this level indicate the utility of the biomarker.

Negative predictive value (NPV): the probability of being a category 2 (intermediate or low responder, or interme-

diately or high responder, depending upon the contrast) individual given that the individual carries the category 2 associated genotype marker. The expected value for NPV given no effect is 75%. Increased departures from this level indicate the utility of the biomarker.

Frequency of the two genotype markers for each biomarker: Values between 15 and 85% for these frequencies indicate a sufficiently frequent marker to be a useful biomarker.

1.3. Results

The purpose of this study was the identification of genetic markers associated to variation of clinical endpoints relevant to growth, herein Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2 annualized and thus reflecting the growth effect of two years of treatment with human recombinant growth hormone in GHD or TS children.

Association with Change in Height in cm from Year 1 to Year 2, Change in Height in cm From Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2

Change in Height in cm from Year 1 to Year 2, Change in Height in cm from Baseline to Year 2, Change in Height SDS from Year 1 to Year 2, Change in Height SDS from Baseline to Year 2 and Height Velocity SDS at Year 2 were considered in this study as the primary markers of growth response.

Association of SNPs in Candidate Genes Through Continuous Analysis

SNPs were tested for association (genotypic, major or minor allele dominance) and the SNPs found to be associated to the above clinical endpoints through these continuous analyses are reported in the Table 5.

Prediction Analysis of SNPs Through Categorical Analysis

Considering categories of response, significant associations were found for GHD children for a number of SNPs as depicted in Tables 3 and 4.

GHD Children

TABLE 3

Marker SNPs in GHD subjects													
Table 3.1 GHD - Change in Height in cm Year 1-2 Tanner stages 1 + 2 only													
		Non-Parametric		Categorical		Categorical		Categorical		Relative Risk		95% CI Relative Risk	
Marker	Gene	Adjusted p-value	Model	Exact p-value	Adjusted p-value	Relative Risk	Number of individuals	Number of individuals	Number of individuals	PPV Frequency of category 1 among carriers of Marker for Category 1	NPV Frequency of Category 2 among carriers of Marker for Category 2		
rs2293152	STAT_cluster	0.044000	Recessive	0.00104	0.00624	6.34	22	37	2	32	0.3729	0.9412	
rs3173908	PIK3CG	0.001700	Recessive	0.00138	0.00966	4.84	21	34	3	35	0.3818	0.9211	
rs4730205	PIK3CG	0.018200	Recessive	0.00173	0.01211	3.72	19	28	5	41	0.4043	0.8913	
rs1801270	CDKN1A	0.044100	Recessive	0.01957	0.01957	2.34	9	9	16	59	0.5000	0.7867	
rs7533750	PIK3R3	0.036600	Recessive	0.00682	0.02046	2.55	14	17	11	51	0.4516	0.8226	
rs1801270	CDKN1A	0.044100	Recessive	0.03487	0.03487	5.52	23	52	1	17	0.3067	0.9444	
rs687088	IGF2R	0.795000	Recessive	0.00034	0.00841	4.23	19	25	5	44	0.4318	0.8980	
rs4645956	MYC	0.480600	Recessive	0.01736	0.03472	4.04	22	46	2	23	0.3235	0.9200	

Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total Frequency	Total Genotype Marker for Category 1	Total Genotype Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	Relative Risk	PPV Frequency of category 1 among carriers of Marker for Category 1	NPV Frequency of Category 2 among carriers of Marker for Category 2	
rs2293152	STAT_cluster	L	I + H	GG & CG	CC	0.6344	0.3656	0.3656	22	37	2	32	0.3729	0.9412
rs3173908	PIK3CG	L	I + H	CC	TT & TC	0.5914	0.4086	0.4086	21	34	3	35	0.3818	0.9211
rs4730205	PIK3CG	L	I + H	CC	TT & TC	0.5054	0.4946	0.4946	19	28	5	41	0.4043	0.8913
rs1801270	CDKN1A	H	I + L	AA & AC	CC	0.1935	0.8065	0.8065	9	9	16	59	0.5000	0.7867
rs7533750	PIK3R3	H	I + L	CC & GC	GG	0.3333	0.6667	0.6667	14	17	11	51	0.4516	0.8226
rs1801270	CDKN1A	L	I + H	CC	AA & AC	0.8065	0.1935	0.1935	23	52	1	17	0.3067	0.9444
rs687088	IGF2R	L	I + H	TT & TC	CC	0.4731	0.5269	0.5269	19	25	5	44	0.4318	0.8980
rs4645956	MYC	L	I + H	CC	TT & TC	0.7312	0.2688	0.2688	22	46	2	23	0.3235	0.9200

Table 3.2 GHD - Change in Height SDS Year 1-2 Tanner stages 1 + 2 only

Marker	Gene	Non-Parametric	Categorical Model	Categorical	Relative Risk	95% CI Relative Risk
		Adjusted p-value		Exact p-value		
rs7536561	LHX4	0.007300	Dominance	0.00142	3.19	[1.72, 5.92]
rs6058189	ID1	0.066500	Recessive	0.03151	3.61	[0.92, 14.21]
rs7960652	PPP1CC	0.296800	Recessive	0.01883	2.27	[1.15, 4.50]
rs827423	ESR1	0.745500	Dominance	0.00100	3.21	[1.66, 6.21]

TABLE 3-continued

Marker SNPs in GHD subjects									
Marker	Gene	Category 1	Category 2	Category 1	Category 2	Category 1	Category 2	Category 1	Category 2
rs7536561	LHX4	H	I + L	AA	GG & AG	0.1828	0.8172	10	7
rs6058189	ID1	H	I + L	AA	GG & AG	0.2473	0.7527	22	48
rs7960552	PPP1CC	L	I + H	TT	CC & TC	0.3978	0.6022	15	22
rs827423	ESR1	H	I + L	AA	GG & AG	0.2688	0.7312	13	12

Table 3.3 GHD - Height velocity SDS Year 2 Tanner Stages 1 + 2 only									
Marker	Gene	Non-Parametric Adjusted p-value		Categorical Exact p-value		Categorical Adjusted p-value		95% CI Relative Risk	
		Category 1		Category 2		Category 1		Category 2	
rs3821799	ADIPOQ	0.023200		0.00062		0.00371		NA	
rs9658584	CYR61	0.054300		0.00323		0.00646		3.31	
rs3842748	INS	0.229800		0.01166		0.01166		3.67	
rs6547874	PPP1CB	1.000000		0.00471		0.03299		4.98	
rs6706858	PPP1CB	1.000000		0.00471		0.03299		4.98	
rs3190	PPP1CB	1.000000		0.00471		0.03299		4.98	
rs12693005	PDK1	0.625700		0.00893		0.04464		2.61	
rs2168043	SOS1	0.204400		0.00908		0.04540		2.69	

Table 3.4 Change in Height in cm baseline - Year 2 Tanner stages 1 + 2 only (AUHTC02Tan)									
Marker	Gene	Non-Parametric Adjusted p-value		Categorical Exact p-value		Categorical Adjusted p-value		95% CI Relative Risk	
		Category 1		Category 2		Category 1		Category 2	
rs3821799	ADIPOQ	TT & TC		0.2366		47		0	
rs9658584	CYR61	CC & CG		0.5385		25		6	
rs3842748	INS	GG		0.3441		40		3	
rs6547874	PPP1CB	AA & AG		0.3118		42		2	
rs6706858	PPP1CB	CC & CG		0.3118		42		2	
rs3190	PPP1CB	AA & AG		0.3118		42		2	
rs12693005	PDK1	CC & TC		0.2151		10		14	
rs2168043	SOS1	AA & AC		0.6739		17		10	

Marker	Gene	Non-Parametric Adjusted p-value		Categorical Exact p-value		Categorical Adjusted p-value		95% CI Relative Risk	
		Category 1		Category 2		Category 1		Category 2	
rs2276048	INPPL1	0.040000		0.02499		0.02499		2.25	
rs2888586	SOS1	0.119000		0.00448		0.02240		5.24	
rs3217862	CCND2	1.000000		0.00172		0.02750		3.09	
rs3805236	GAB1	0.103500		0.00387		0.03092		2.89	

TABLE 3-continued

Marker SNPs in GHD subjects													
Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total		Number of		Number of		PPV	NPV
						Frequency Genotype Marker for Category 1	Frequency Genotype Marker for Category 2	Category 1 individuals that Carry Genotype Marker for Category 1	Category 2 individuals that Carry Genotype Marker for Category 2	Category 1 individuals that Carry Genotype Marker for Category 1	Category 2 individuals that Carry Genotype Marker for Category 2	Frequency of category 1 among carriers of Marker for Category 1	Frequency of category 2 among carriers of Marker for Category 2
rs7677000	PPARGC1A			0.169500		Recessive		0.00157		0.03610		3.05	[1.57, 5.91]
rs2168043	SOS1			0.070800		Recessive		0.00908		0.04540		2.69	[1.33, 5.41]
rs2276048	INPPL1	H	I + L	GG & AG	AA	0.3441	0.6559	13	19	11	50	0.4063	0.8197
rs2888586	SOS1	H	I + L	TT & TC	CC	0.6774	0.3226	22	41	2	28	0.3492	0.9333
rs3217862	CCND2	H	I + L	GG & TG	TT	0.3118	0.6882	14	15	10	54	0.4828	0.8438
rs3805236	GAB1	H	I + L	GG	AA & AG	0.4086	0.5914	16	22	8	47	0.4211	0.8545
rs7677000	PPARGC1A	H	I + L	TT & TC	CC	0.2796	0.7204	13	13	11	56	0.5000	0.8358
rs2168043	SOS1	H	I + L	AA & AC	CC	0.3261	0.6739	13	17	10	52	0.4333	0.8387

Table 3.5 Change in Height SDS baseline - Year 2 Tanner stages 1 + 2 only (AUHSDC02Tan)

Marker	Gene	Non-Parametric		Categorical Model	Categorical		Relative Risk	95% CI Relative Risk					
		Adjusted p-value	Exact p-value		Adjusted p-value								
rs9658584	CYR61	0.028700	0.00795	Recessive	0.01590	2.83	[1.30, 6.17]						
rs2960266	SH2B2	0.622300	0.00493	Recessive	0.02463	2.80	[1.41, 5.57]						
rs7677000	PPARGC1A	0.792700	0.00157	Recessive	0.03610	3.05	[1.57, 5.91]						
Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total		Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	PPV Frequency of category 1 among carriers of Marker for Category 1	NPV Frequency of category 2 among carriers of Marker for Category 2		
						Frequency	Frequency						
						Genotype Marker for Category 1	Genotype Marker for Category 2						
						Category 1	Category 2						
						Category 1	Category 2						
rs9658584	CYR61	L	I + H	CC & CG	GG	0.4615	0.5385	17	25	7	42	0.4048	0.8571
rs2960266	SH2B2	H	I + L	CC	TT & TC	0.3333	0.6667	14	17	10	52	0.4516	0.8387
rs7677000	PPARGC1A	H	I + L	TT & TC	CC	0.2796	0.7204	13	13	11	56	0.5000	0.8358

Legend:

Non-parametric adjusted p-value, p-value from Kruskal-Wallis One Way Analysis of Variance by Rank Test adjusted for number of LD blocks tested within the gene.

Categorical models: Dominance test compares carriers of major allele (MaMa or MaMi genotypes) against non-carriers of major allele (MaMi or MaMi genotypes); recessive test compares carriers of minor allele (MaMi or MaMi genotypes) against non-carriers of minor allele (MaMa genotype).

Categorical exact p-value, p-value from Fisher's Exact Test.

Categorical adjusted p-values, p-value from Fisher's Exact Test adjusted by number of LD blocks tested within the gene.

Relative Risk, increased probability of being a Category 1 responder for carriers of the marker genotype compared to carriers of the non-marker genotype.

95% CI Relative Risk, interval within which the true relative risk will lie at a probability of 95%.

Positive Predictive Value (PPV), proportion of Category 1 responders that carry the marker genotype.

Negative Predictive Value (NPV), proportion of Category 2 responders that carry the non-marker genotype.

Carrying the CC genotype for rs2293152 in the STAT gene cluster has a 94% predictive value in GHD children for intermediate or high response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the TT or TC genotype for rs3173908 in the PIK3CG gene has a 92% predictive value in GHD children for intermediate or high response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the CC genotype for rs4730205 in the PIK3CG gene has a 40% predictive value in GHD children for low response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the AA or AC genotype for rs1801270 in the CDKN1A gene has a 50% predictive value in GHD children for high response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the AA or AC genotype for rs1801270 in the CDKN1A gene has a 94% predictive value in GHD children for intermediate or high response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the CC or CG genotype for rs7533750 in the PIK3R3 gene has a 45% predictive value in GHD children for high response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the AA genotype for rs7536561 in the LHX4 gene has a 59% predictive value in GHD children for high response based on the Change in Height SDS from Year 1 to Year 2.

Carrying the CC genotype for rs3821799 in the ADIPOQ gene has a 100% predictive value in GHD children for intermediate or low response based on Height Velocity SDS at Year 2.

Carrying the TT or TC genotype for rs687088 in the IGF2R gene has a 43% predictive value in GHD children for low response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the TT or TC genotype for rs4645956 in the MYC gene has a 92% predictive value in GHD children for intermediate or high response based on the Change in Height in cm from Year 1 to Year 2.

Carrying the GG or AG genotype for rs2276048 in the INPPL1 gene has a 41% predictive value in GHD children for high response based on the Change in Height in cm from Baseline to Year 2.

Carrying the CC genotype for rs2888586 in the SOS1 gene has a 93% predictive value in GHD children for intermediate or low response based on the Change in Height in cm from Baseline to Year 2.

Carrying the AA or AC genotype for rs2168043 in the SOS1 gene has a 43% predictive value in GHD children for high response based on the Change in Height in cm from Baseline to Year 2.

Carrying the GG or TG genotype for rs3217862 in the CCND2 gene has a 48% predictive value in GHD children for high response based on the Change in Height in cm from Baseline to Year 2.

Carrying the GG genotype for rs3805236 in the GAB1 gene has a 42% predictive value in GHD children for high response based on the Change in Height in cm from Baseline to Year 2.

Carrying the TT or TC genotype for rs7677000 in the PPARGC1A gene has a 50% predictive value in GHD children for high response based on the Change in Height in cm from Baseline to Year 2.

Carrying the GG or AG genotype for rs6058189 in the ID1 gene has a 91% predictive value in GHD children for intermediate or low response based on the Change in Height SDS from Year 1 to Year 2.

Carrying the TT genotype for rs7960552 in the PPP1CC gene has a 41% predictive value in GHD children for low response based on the Change in Height SDS from Year 1 to Year 2.

Carrying the AA genotype for rs827423 in the ESR1 gene has a 52% predictive value in GHD children for high response based on the Change in Height SDS from Year 1 to Year 2.

Carrying the CC or CG genotype for rs9658584 in the CYR61 gene has a 40% predictive value in GHD children for low response based on the Change in Height SDS from Baseline to Year 2.

Carrying the CC genotype for rs2960266 in the SH2B2 gene has a 45% predictive value in GHD children for high response based on the Change in Height SDS from Baseline to Year 2.

Carrying the TT or TC genotype for rs7677000 in the PPARGC1A gene has a 50% predictive value in GHD children for high response based on the Change in Height SDS from Baseline to Year 2.

Carrying the CC or CG genotype for rs9658584 in the CYR61 gene has a 40% predictive value in GHD children for low response based on the Height Velocity SDS at Year 2.

Carrying the CC or CG genotype for rs3842748 in the INS gene has a 91% predictive value in GHD children for intermediate or low response based on Height Velocity SDS at Year 2.

Carrying the GG genotype for rs6547874 in the PPP1CB gene has a 93% predictive value in GHD children for intermediate or high response based on Height Velocity SDS at Year 2.

Carrying the GG genotype for rs6706858 in the PPP1CB gene has a 93% predictive value in GHD children for intermediate or high response based on Height Velocity SDS at Year 2.

Carrying the GG genotype for rs3190 in the PPP1CB gene has a 93% predictive value in GHD children for intermediate or high response based on Height Velocity SDS at Year 2.

Carrying the CC or TC genotype for rs12693005 in the PDK1 gene has a 50% predictive value in GHD children for high response based on Height Velocity SDS at Year 2.

Carrying the AA or AC genotype for rs2168043 in the SOS1 gene has a 43% predictive value in GHD children for high response based on Height Velocity SDS at Year 2.

TS Children

TABLE 4

Marker SNPs in TS subjects

Table 4.1 TS - Change in Height in cm Year 1-2 Tanner stages 1 + 2 only

Marker	Gene	Non-Parametric Adjusted p-value	Categorical Model	Categorical Exact p-value	Categorical Adjusted p-value	Relative Risk	95% CI Relative Risk
rs5906709	GATA1	0.014400	Recessive	0.02094	0.02094	3.38	[1.29, 8.90]
rs3817899	IGFALS	0.014800	Recessive	0.03761	0.03761	3.06	[1.21, 7.75]
rs2278914	SOS1	0.040800	Recessive	0.01292	0.03875	4.13	[1.56, 10.88]
rs3787335	PTPN1	0.026500	Recessive	0.00556	0.03894	4.38	[1.56, 12.26]
rs1151996	PPARG	0.393800	Recessive	0.00116	0.00810	NA	NA
rs709149	PPARG	0.393800	Recessive	0.00116	0.00810	NA	NA
rs1175540	PPARG	0.725900	Recessive	0.00116	0.00810	NA	NA

Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total Frequency Marker for Category 1	Total Frequency Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	PPV Frequency of category 1 among carriers of Marker for Category 1	NPV Frequency of category 2 among carriers of Marker for Category 2
rs5906709	GATA1	H	I + L	G allele	A- or AA	0.2619	0.7381	6	5	5	26	0.5455	0.8387
rs3817899	IGFALS	H	I + L	CC & CG	GG	0.2143	0.7857	5	4	6	27	0.5556	0.8182
rs2278914	SOS1	H	I + L	GG & AG	AA	0.1951	0.8049	5	3	5	28	0.6250	0.8485
rs3787335	PTPN1	L	I + H	GG & TG	TT	0.2857	0.7143	7	5	4	26	0.5833	0.8667
rs1151996	PPARG	L	I + H	CC & AC	AA	0.5952	0.4048	11	14	0	17	0.4400	1.0000
rs709149	PPARG	L	I + H	AA & AG	GG	0.5952	0.4048	11	14	0	17	0.4400	1.0000
rs1175540	PPARG	L	I + H	AA & AC	CC	0.5952	0.4048	11	14	0	17	0.4400	1.0000

Table 4.2 TS - Height velocity SDS Year 2 Tanner stages 1 + 2 only

Marker	Gene	Non-Parametric Adjusted p-value	Categorical Model	Categorical Exact p-value	Categorical Adjusted p-value	Relative Risk	95% CI Relative Risk
rs751210	SLC2A1	0.048400	Recessive	0.00397	0.03177	6.00	[1.47, 24.45]
rs4655537	LEPR	1.000000	Recessive	0.00020	0.00428	NA	NA
rs989634	SREBF1	0.116500	Dominance	0.00851	0.00851	4.17	[1.75, 9.91]
rs5906709	GATA1	0.183400	Recessive	0.02094	0.02094	3.38	[1.29, 8.90]
rs2276048	INPPL1	0.058700	Recessive	0.02391	0.02391	3.50	[1.23, 9.98]
rs13041704	PTPN1	0.376800	Recessive	0.00348	0.02433	NA	NA
rs2069840	IL6	0.057900	Recessive	0.02891	0.02891	3.92	[1.21, 12.70]
rs2069408	CDK2	0.278800	Recessive	0.03532	0.03532	4.09	[1.00, 16.71]
rs4151551	RB1	0.194200	Recessive	0.00925	0.03700	NA	NA
rs4802071	AKT2	0.448400	Recessive	0.04264	0.04264	3.23	[0.99, 10.50]

TABLE 4-continued

Marker SNPs in TS subjects											
Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total Frequency Marker for Category 1	Total Frequency Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2
rs751210	SLC2A1	H	I + L	AA & AG	GG	0.4286	0.5714	9	9	2	22
rs4655537	LEPR	L	I + H	AA & AG	GG	0.5238	0.4762	11	11	0	20
rs9899634	SREBF1	H	I + L	TT	AA & TA	0.1667	0.8333	5	2	6	29
rs5906709	GATA1	H	I + L	G allele, G ₊ , GG or AG	A ₊ , AA	0.2619	0.7381	6	5	5	26
rs2276048	INPPL1	H	I + L	GG & AG	AA	0.3333	0.6667	7	7	4	24
rs13041704	PTPN1	L	I + H	CC & AC	AA	0.6429	0.3571	11	16	0	15
rs2069840	IL6	H	I + L	GG & GC	CC	0.4048	0.5952	8	9	3	22
rs2069408	CDK2	H	I + L	GG & AG	AA	0.5238	0.4762	9	13	2	18
rs4151551	RB1	H	I + L	GG	TT & TG	0.6905	0.3095	11	18	0	13
rs4802071	AKT2	H	I + L	TT	CC & TC	0.4524	0.5476	8	11	3	20

Table 4.3 Change in Height in cm baseline - Year 2 Tanner stages 1 + 2 only (AUHTC02Tan)

Marker	Gene	Non-Parametric		Categorical		Relative Risk	95% CI Relative Risk
		Adjusted p-value	Model	Exact p-value	Adjusted p-value		
rs3787335	PTPN1	0.030200	Recessive	0.00556	0.03894	4.38	[1.56, 12.26]
rs2149556	JAK2	0.566300	Dominance	0.00261	0.02345	4.93	[1.78, 13.65]
rs7034753	JAK2	0.481100	Dominance	0.00261	0.02345	4.93	[1.78, 13.65]
rs751210	SLC2A1	1.000000	Recessive	0.00397	0.03177	6.00	[1.47, 24.45]
rs7046736	JAK2	0.259300	Recessive	0.00397	0.03574	6.00	[1.47, 24.45]
rs7043371	JAK2	0.701400	Dominance	0.00501	0.04512	4.40	[1.74, 11.15]
rs4460309	PIK3CG	0.381900	Recessive	0.01584	0.04753	6.80	[0.96, 48.33]

TABLE 4-continued

Marker SNPs in TS subjects													
Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total Frequency Genotype Marker for Category 1	Total Frequency Genotype Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	PPV Frequency of category 1 among carriers of Marker for Category 1	NPV Frequency of Category 2 among carriers of Marker for Category 2
rs3787335	PTPN1	L	I + H	GG & TG	TT	0.2857	0.7143	7	5	4	26	0.5833	0.8667
rs2149556	JAK2	H	I + L	TT	CC & TC	0.2619	0.7381	7	4	4	27	0.6364	0.8710
rs7034753	JAK2	H	I + L	GG	AA & AG	0.2619	0.7381	7	4	4	27	0.6364	0.8710
rs751210	SLC2A1	H	I + L	AA & AG	GG	0.4286	0.5714	9	9	2	22	0.5000	0.9167
rs7046736	JAK2	H	I + L	AA & AC	CC	0.4286	0.5714	9	9	2	22	0.5000	0.9167
rs7043371	JAK2	H	I + L	AA	TT & TA	0.2143	0.7857	6	3	5	28	0.6667	0.8485
rs4460309	PIK3CG	H	I + L	CC	TT & TC	0.5952	0.4048	10	15	1	16	0.4000	0.9412

Table 4.4 Change in Height SDS Year 1-2 Tanner stages 1 + 2 only (AUHSDC12Tan)							
Marker	Gene	Non-Parametric Adjusted p-value	Categorical Model	Categorical Exact p-value	Categorical Adjusted p-value	Relative Risk	95% CI Relative Risk
rs5906709	GATA1	0.059000	Recessive	0.02094	0.02094	3.38	[1.29, 8.90]
rs3817899	IGFALS	0.187400	Recessive	0.04131	0.04131	NA	NA

Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total Frequency Genotype Marker for Category 1	Total Frequency Genotype Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	Number of individuals that Carry Genotype Marker for Category 1	Number of individuals that Carry Genotype Marker for Category 2	ppv Frequency of category 1 among carriers of Marker for Category 1	NPV Frequency of Category 2 among carriers of Marker for Category 2
rs5906709	GATA1	H	I + L	G allele, G ₁ , GG or AG	A-, or AA	0.2619	0.7381	6	5	5	26	0.5455	0.8387
rs3817899	IGFALS	L	I + H	GG	CC & CG	0.7857	0.2143	12	21	0	9	0.3636	1.0000

Table 4.5 Change in Height SDS baseline - Year 2 Tanner stages 1 + 2 only (AUHSDC02Tan)							
Marker	Gene	Non-Parametric Adjusted p-value	Categorical Model	Categorical Exact p-value	Categorical Adjusted p-value	Relative Risk	95% CI Relative Risk
rs3787335	PTPN1	0.007100	Recessive	0.00049	0.00345	6.67	[2.12, 20.96]
rs13041704	PTPN1	0.415400	Recessive	0.00348	0.02433	NA	NA
rs2069502	CDK4	0.776500	Recessive	0.01584	0.03169	6.80	[0.96, 48.33]
rs7981705	IRS2	0.699100	Recessive	0.00547	0.04373	5.03	[1.54, 16.38]
rs4460309	PIK3CG	0.641600	Recessive	0.01584	0.04753	6.80	[0.96, 48.33]

TABLE 4-continued

Marker SNPs in TS subjects												
Marker	Gene	Category 1	Category 2	Genotype Marker for Category 1	Genotype Marker for Category 2	Total Frequency Genotype Marker for Category 1	Total Frequency Genotype Marker for Category 2	Number of Category 1 individuals that Carry Genotype Marker for Category 1	Number of Category 2 individuals that Carry Genotype Marker for Category 2	Number of Category 1 individuals that Carry Genotype Marker for Category 2	NPV Frequency of Category 2 among carriers of Marker for Category 2	
rs3787335	PTPN1	L	I + H	GG & TG	TT	0.2857	0.7143	8	4	3	0.6667	0.9000
rs13041704	PTPN1	L	I + H	CC & AC	AA	0.6429	0.3571	11	16	0	0.4074	1.0000
rs2069502	CDK4	L	I + H	TT & TC	CC	0.5952	0.4048	10	15	1	0.4000	0.9412
rs7981705	IRS2	L	I + H	TT & TC	CC	0.3171	0.6829	7	6	3	0.5385	0.8929
rs4460309	PIK3CG	H	I + L	CC	TT & TC	0.5952	0.4048	10	15	1	0.4000	0.9412

Legend:
Non-parametric adjusted p-value, p-value from Kruskal-Wallis One Way Analysis of Variance by Rank Test adjusted for number of LD blocks tested within the gene.
Categorical models: Dominance test compares carriers of major allele (MaMa or MaMi genotypes) against non-carriers of major allele (MiMi genotype); recessive test compares carriers of minor allele (MaMi or MiMi genotypes) against non-carriers of minor allele (MaMa genotype).
Categorical exact p-value, p-value from Fisher's Exact Test.
Categorical adjusted p-values, p-value from Fisher's Exact Test adjusted by number of LD blocks tested within the gene.
Relative Risk, increased probability of being a Category 1 responder for carriers of the marker genotype compared to carriers of the non-marker genotype.
95% CI Relative Risk, interval within which the true relative risk will lie at a probability of 95%.
Positive Predictive Value (PPV), proportion of Category 1 responders that carry the marker genotype.
Negative Predictive Value (NPV), proportion of Category 2 responders that carry the non-marker genotype.

Carrying the G allele (G_, GG or GA genotype) for rs5906709 in the GATA1 gene has a 55% predictive value in TS Girls for high response based on Change in Height in cm from Year 1 to Year 2.

Carrying the CC or CG genotype for rs3817899 in the IGFALS gene has a 56% predictive value in TS Girls for high response based on Change in Height in cm from Year 1 to Year 2.

Carrying the GG or AG genotype for rs2278914 in the SOS1 gene has a 63% predictive value in TS Girls for high response based on Change in Height in cm from Year 1 to Year 2.

Carrying the GG or TG genotype for rs3787335 in the PTPN1 gene has a 58% predictive value in TS Girls for low response based on Change in Height in cm from Year 1 to Year 2.

Carrying the AA or AG genotype for rs751210 in the SLC2A1 gene has a 50% predictive value in TS Girls for high response based on Height Velocity SDS at Year 2.

Carrying the GG genotype for rs751210 in the SLC2A1 gene has a 92% predictive value in TS Girls for intermediate or low response based on Height Velocity SDS at Year 2.

Carrying the CC & AC genotype for rs1151996 in the PPARG gene has a 44% predictive value in TS Girls for low response based on Change in Height in cm from Year 1 to Year 2.

Carrying the AA genotype for rs1151996 in the PPARG gene has a 100% predictive value in TS Girls for intermediate or high response based on Change in Height in cm from Year 1 to Year 2.

Carrying the AA pr AG genotype for rs709149 in the PPARG gene has a 44% predictive value in TS Girls for low response based on Change in Height in cm from Year 1 to Year 2.

Carrying the GG genotype for rs709149 in the PPARG gene has a 100% predictive value in TS Girls for intermediate or high response based on Change in Height in cm from Year 1 to Year 2.

Carrying the AA pr AC genotype for rs1175540 in the PPARG gene has a 44% predictive value in TS Girls for low response based on Change in Height in cm from Year 1 to Year 2.

Carrying the CC genotype for rs1175540 in the PPARG gene has a 100% predictive value in TS Girls for intermediate or high response based on Change in Height in cm from Year 1 to Year 2.

Carrying the GG or TG genotype for rs3787335 in the PTPN1 gene has a 58% predictive value in TS Girls for low response based on Change in Height in cm from Baseline to Year 2.

Carrying the TT genotype for rs2149556 in the JAK2 gene has a 64% predictive value in TS

Girls for high response based on Change in Height in cm from Baseline to Year 2.

Carrying the GG genotype for rs7034753 in the JAK2 gene has a 64% predictive value in TS Girls for high response based on Change in Height in cm from Baseline to Year 2.

Carrying the AA or AC genotype for rs7046736 in the JAK2 gene has a 50% predictive value in TS Girls for high response based on Change in Height in cm from Baseline to Year 2.

Carrying the CC genotype for rs7046736 in the JAK2 gene has a 92% predictive value in TS Girls for intermediate or low response based on Change in Height in cm from Baseline to Year 2.

Carrying the AA genotype for rs7043371 in the JAK2 gene has a 67% predictive value in TS Girls for high response based on Change in Height in cm from Baseline to Year 2.

Carrying the AA or AG genotype for rs751210 in the SLC2A1 gene has a 50% predictive value in TS Girls for high response based on Change in Height in cm from Baseline to Year 2.

Carrying the GG genotype for rs751210 in the SLC2A1 gene has a 92% predictive value in TS Girls for intermediate or low response based on Change in Height in cm from Baseline to Year 2.

Carrying the TT or TC genotype for rs4460309 in the PIK3CG gene has a 94% predictive value in TS Girls for intermediate or low response based on Change in Height in cm from Baseline to Year 2.

Carrying the CC genotype for rs4460309 in the PIK3CG gene has a 40% predictive value in TS Girls high response based on Change in Height in cm from Baseline to Year 2.

Carrying the G allele (G_, GG or GA genotype) for rs5906709 in the GATA1 gene has a 55% predictive value in TS Girls for high response based on Change in Height SDS from Year 1 to Year 2.

Carrying the CC or CG genotype for rs3817899 in the IGFALS gene has a 100% predictive value in TS Girls for intermediate or high response based on Change in Height SDS from Year 1 to Year 2.

Carrying the GG or TG genotype for rs3787335 in the PTPN1 gene has a 67% predictive value in TS Girls for low response based on Change in Height SDS from Baseline to Year 2.

Carrying the TT genotype for rs3787335 in the PTPN1 gene has a 90% predictive value in TS Girls for intermediate or high response based on Change in Height SDS from Baseline to Year 2.

Carrying the CC or CA genotype for rs13041704 in the PTPN1 gene has a 41% predictive value in TS Girls for low response based on Change in Height SDS from Baseline to Year 2.

Carrying the AA genotype for rs13041704 in the PTPN1 gene has a 100% predictive value in TS Girls for intermediate or high response based on Change in Height SDS from Baseline to Year 2.

Carrying the CC genotype for rs2069502 in the CDK4 gene has a 94% predictive value in TS Girls for intermediate or high response based on Change in Height SDS from Baseline to Year 2.

Carrying the TT or TC genotype for rs7981705 in the IRS2 gene has a 54% predictive value in TS Girls for low response based on Change in Height SDS from Baseline to Year 2.

Carrying the TT or TC genotype for rs4460309 in the PIK3CG gene has a 94% predictive value in TS Girls for intermediate or low response based on Change in Height SDS from Baseline to Year 2.

Carrying the AA or AG genotype for rs4655537 in the LEPR gene has a 50% predictive value in TS Girls for low response based on Height Velocity SDS at Year 2.

Carrying the GG genotype for rs4655537 in the LEPR gene has a 100% predictive value in TS Girls for intermediate or high response based on Height Velocity SDS at Year 2.

Carrying the TT genotype for rs9899634 in the SREBF1 gene has a 71% predictive value in TS Girls for high response based on Height Velocity SDS at Year 2.

Carrying the G allele (G_, GG or GA genotype) for rs5906709 in the GATA1 gene has a 55% predictive value in TS Girls for high response based on Height Velocity SDS at Year 2.

Carrying the GG or AG genotype for rs2276048 in the INPL1 gene has a 50% predictive value in TS Girls for high response based on Height Velocity SDS at Year 2.

Carrying the CC or AC genotype for rs13041704 in the PTPN1 gene has a 41% predictive value in TS Girls for low response based on Height Velocity SDS at Year 2.

Carrying the AA genotype for rs13041704 in the PTPN1 gene has a 100% predictive value in TS Girls for intermediate or high response based on Height Velocity SDS at Year 2.

Carrying the GG or GC genotype for rs2069840 in the IL6 gene has a 47% predictive value in TS Girls for high response based on Height Velocity SDS at Year 2.

Carrying the GG or AG genotype for rs2069408 in the CDK2 gene has a 41% predictive value in TS Girls for high response based on Height Velocity SDS at Year 2.

Carrying the AA genotype for rs2069408 in the CDK2 gene has a 90% predictive value in TS Girls for intermediate or low response based on Height Velocity SDS at Year 2.

Carrying the TT or TG genotype for rs4151551 in the RB1 gene has a 100% predictive value in TS Girls for intermediate or low response based on Height Velocity SDS at Year 2.

Carrying the TT genotype for rs4802071 in the AKT2 gene has a 42% predictive value in TS Girls for high response based on Height Velocity SDS at Year 2.

TABLE 5

Associated SNPs through Continuous analyses											
SNP ID	Gene	Nb Markers in Gene	Quantitative Variable	Gender	Disease	Nb LD Blocks	Association Tested	Nominal p-value	Adjusted p-value	Minor Allele Frequency	Call Rate
rs3173908	PIK3CG	9	Height (cm) Change from Year 1 to Year 2	NA	GHD	7	Minor allele presence	0.000236	0.0017	22.0%	100.00%
rs7101	FOS	2	Height SDS Change from Baseline to Year 2	NA	GHD	2	Major allele presence	0.001935	0.0039	24.5%	99.01%
rs8017367	SOS2	10	Height SDS Change from Baseline to Year 2	NA	GHD	8	Minor allele presence	0.000556	0.0045	28.5%	100.00%
rs3173908	PIK3CG	9	Height (cm) Change from Year 1 to Year 2	NA	GHD	7	Genotype	0.000893	0.0063	22.0%	100.00%
rs7101	FOS	2	Height (cm) Change from Baseline to Year 2	NA	GHD	2	Major allele presence	0.003631	0.0073	24.5%	99.01%
rs2895543	SHOX	1	Height SDS Change from Baseline to Year 2	NA	GHD	1	Genotype	0.008076	0.0081	20.4%	100.00%
rs9302989	GRB2	6	Height (cm) Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.003019	0.0091	23.1%	100.00%
rs3828942	LEP	6	Height Velocity SDS at Year 2	NA	GHD	4	Genotype	0.002372	0.0095	46.8%	100.00%
rs1130214	AKT1	3	Height (cm) Change from Year 1 to Year 2	NA	GHD	1	Minor allele presence	0.011974	0.012	30.1%	100.00%
rs7101	FOS	2	Height (cm) Change from Baseline to Year 2	NA	GHD	2	Genotype	0.006775	0.0136	24.5%	99.01%
rs7101	FOS	2	Height SDS Change from Baseline to Year 2	NA	GHD	2	Genotype	0.007209	0.0144	24.5%	99.01%
rs2909430	TP53	6	Height SDS Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.005019	0.0151	15.6%	100.00%
rs10244329	LEP	6	Height Velocity SDS at Year 2	NA	GHD	4	Genotype	0.003903	0.0156	46.8%	100.00%
rs1026825	BCL2	122	Height Velocity SDS at Year 2	NA	GHD	43	Major allele presence	0.000408	0.0175	48.9%	100.00%
rs4730205	PIK3CG	9	Height (cm) Change from Year 1 to Year 2	NA	GHD	7	Minor allele presence	0.002593	0.0182	28.0%	100.00%
rs4771644	IRS2	14	Height Velocity SDS at Year 2	NA	GHD	10	Genotype	0.001931	0.0193	47.3%	99.01%
rs8017367	SOS2	10	Height SDS Change from Baseline to Year 2	NA	GHD	8	Genotype	0.002547	0.0204	28.5%	100.00%
rs3821799	ADIPOQ	11	Height Velocity SDS at Year 2	NA	GHD	6	Minor allele presence	0.003871	0.0232	49.5%	100.00%
rs4771644	IRS2	14	Height Velocity SDS at Year 2	NA	GHD	10	Minor allele presence	0.002334	0.0233	47.3%	99.01%
rs7101	FOS	2	Height Velocity SDS at Year 2	NA	GHD	2	Major allele presence	0.012296	0.0246	24.5%	99.01%
rs5906709	GATA1	1	Height SDS Change from Baseline to Year 2	Boys	GHD	1	Major allele presence	0.027265	0.0273	20.7%	100.00%
rs5906709	GATA1	1	Height SDS Change from Baseline to Year 2	Boys	GHD	1	Genotype	0.027265	0.0273	20.7%	100.00%
rs5906709	GATA1	1	Height SDS Change from Baseline to Year 2	Boys	GHD	1	Minor allele presence	0.027265	0.0273	20.7%	100.00%
rs12495941	ADIPOQ	11	Height (cm) Change from Baseline to Year 2	NA	GHD	6	Major allele presence	0.004727	0.0284	35.5%	100.00%
rs9658584	CYR61	2	Height SDS Change from Baseline to Year 2	NA	GHD	2	Minor allele presence	0.014357	0.0287	26.4%	98.02%
rs2276048	INPL1	2	Height Velocity SDS at Year 2	NA	GHD	1	Minor allele presence	0.028699	0.0287	18.8%	100.00%
rs10244329	LEP	6	Height Velocity SDS at Year 2	NA	GHD	4	Major allele presence	0.007551	0.0302	46.8%	100.00%

TABLE 5-continued

Associated SNPs through Continuous analyses											
SNP ID	Gene	Nb Markers in Gene	Quantitative Variable	Gender	Disease	Nb LD Blocks	Association Tested	Nominal p-value	Adjusted p-value	Minor Allele Frequency	Call Rate
rs8079197	GRB2	6	Height (cm) Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.010624	0.0319	28.5%	100.00%
rs2289046	IRS2	14	Height (cm) Change from Baseline to Year 2	NA	GHD	10	Major allele presence	0.003306	0.0331	28.3%	99.01%
rs8079197	GRB2	6	Height SDS Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.011349	0.034	28.5%	100.00%
rs7101	FOS	2	Height Velocity SDS at Year 2	NA	GHD	2	Genotype	0.017702	0.0354	24.5%	99.01%
rs1130214	AKT1	3	Height (cm) Change from Year 1 to Year 2	NA	GHD	1	Genotype	0.036009	0.036	30.1%	100.00%
rs7533750	PIK3R3	9	Height (cm) Change from Year 1 to Year 2	NA	GHD	3	Minor allele presence	0.012206	0.0366	19.4%	100.00%
rs9302989	GRB2	6	Height (cm) Change from Baseline to Year 2	NA	GHD	3	Genotype	0.012297	0.0369	23.1%	100.00%
rs7536561	LHX4	26	Height Velocity SDS at Year 2	NA	GHD	22	Major allele presence	0.001741	0.0383	46.8%	100.00%
rs2276048	INPPL1	2	Height (cm) Change from Baseline to Year 2	NA	GHD	1	Minor allele presence	0.039958	0.04	18.8%	100.00%
rs2895543	SHOX	1	Height SDS Change from Baseline to Year 2	NA	GHD	1	Major allele presence	0.040827	0.0408	20.4%	100.00%
rs4789186	GRB2	6	Height (cm) Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.013817	0.0415	23.7%	100.00%
rs2909430	TP53	6	Height (cm) Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.014127	0.0424	15.6%	100.00%
rs2293152	STAT_cluster	10	Height (cm) Change from Year 1 to Year 2	NA	GHD	6	Major allele presence	0.007335	0.044	38.7%	100.00%
rs1801270	CDKN1A	4	Height (cm) Change from Year 1 to Year 2	NA	GHD	1	Minor allele presence	0.044117	0.0441	10.8%	100.00%
rs9302989	GRB2	6	Height (cm) Change from Year 1 to Year 2	NA	GHD	3	Minor allele presence	0.014798	0.0444	23.1%	100.00%
rs3110697	IGFBP3	7	Height SDS Change from Baseline to Year 2	NA	GHD	6	Major allele presence	0.007891	0.0473	34.2%	99.01%
rs9302989	GRB2	6	Height SDS Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.015791	0.0474	23.1%	100.00%
rs2267922	PIK3R2	9	Height (cm) Change from Year 1 to Year 2	NA	GHD	1	Genotype	0.047913	0.0479	48.9%	100.00%
rs2073115	IRS4	1	Height (cm) Change from Year 1 to Year 2	Girls	GHD	1	Genotype	0.048415	0.0484	31.4%	99.01%
rs3828942	LEP	6	Height Velocity SDS at Year 2	NA	GHD	4	Minor allele presence	0.012231	0.0489	46.8%	100.00%
rs4789182	GRB2	6	Height (cm) Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.016332	0.049	29.6%	100.00%
rs4789182	GRB2	6	Height SDS Change from Baseline to Year 2	NA	GHD	3	Minor allele presence	0.01633	0.049	29.6%	100.00%
rs2168043	SOS1	49	Height SDS Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.001363	0.0041	17.9%	100.00%
rs751210	SLC2A1	14	Height Velocity SDS at Year 2	NA	TS	8	Genotype	0.000681	0.0054	25.0%	100.00%
rs3787335	PTPN1	17	Height SDS Change from Baseline to Year 2	NA	TS	7	Genotype	0.001016	0.0071	14.3%	100.00%
rs3787335	PTPN1	17	Height SDS Change from Baseline to Year 2	NA	TS	7	Minor allele presence	0.001016	0.0071	14.3%	100.00%
rs2297141	CYR61	2	Height Velocity SDS at Year 2	NA	TS	2	Minor allele presence	0.004877	0.0098	41.5%	95.92%
rs7127461	ARRB1	22	Height (cm) Change from Year 1 to Year 2	NA	TS	19	Minor allele presence	0.000629	0.0119	21.4%	100.00%
rs2168043	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.004315	0.0129	17.9%	100.00%
rs5906709	GATA1	1	Height (cm) Change from Year 1 to Year 2	NA	TS	1	Minor allele presence	0.014448	0.0144	20.2%	100.00%
rs3817899	IGFALS	1	Height (cm) Change from Year 1 to Year 2	NA	TS	1	Minor allele presence	0.014812	0.0148	11.9%	100.00%
rs809775	PIK3R3	4	Height Velocity SDS at Year 2	NA	TS	2	Minor allele presence	0.008382	0.0168	50.0%	100.00%
rs2168043	SOS1	49	Height SDS Change from Baseline to Year 2	NA	TS	3	Genotype	0.005886	0.0177	17.9%	100.00%
rs6758330	SOS1	49	Height SDS Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.006581	0.0197	13.1%	100.00%
rs11674846	SOS1	49	Height SDS Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.006581	0.0197	13.1%	100.00%
rs2060987	SOS1	49	Height SDS Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.006581	0.0197	13.1%	100.00%

TABLE 5-continued

Associated SNPs through Continuous analyses											
SNP ID	Gene	Nb Markers in Gene	Quantitative Variable	Gender	Disease	Nb LD Blocks	Association Tested	Nominal p-value	Adjusted p-value	Minor Allele Frequency	Call Rate
rs2060988	SOS1	49	Height SDS Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.006581	0.0197	13.1%	100.00%
rs1454219	SOS1	49	Height SDS Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.006581	0.0197	13.1%	100.00%
rs3817899	IGFALS	1	Height (cm) Change from Baseline to Year 2	NA	TS	1	Minor allele presence	0.02624	0.0262	11.9%	100.00%
rs3787335	PTPN1	17	Height (cm) Change from Year 1 to Year 2	NA	TS	7	Genotype	0.003784	0.0265	14.3%	100.00%
rs3787335	PTPN1	17	Height (cm) Change from Year 1 to Year 2	NA	TS	7	Minor allele presence	0.003784	0.0265	14.3%	100.00%
rs809775	PIK3R3	4	Height SDS Change from Baseline to Year 2	NA	TS	2	Minor allele presence	0.013587	0.0272	50.0%	100.00%
rs4845401	SHC1	2	Height Velocity SDS at Year 2	NA	TS	1	Minor allele presence	0.027713	0.0277	47.6%	100.00%
rs5906709	GATA1	1	Height (cm) Change from Year 1 to Year 2	NA	TS	1	Genotype	0.029895	0.0299	20.2%	100.00%
rs3787335	PTPN1	17	Height (cm) Change from Baseline to Year 2	NA	TS	7	Genotype	0.004315	0.0302	14.3%	100.00%
rs3787335	PTPN1	17	Height (cm) Change from Baseline to Year 2	NA	TS	7	Minor allele presence	0.004315	0.0302	14.3%	100.00%
rs2278914	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.011295	0.0339	11.0%	97.96%
rs11263591	FGF3	2	Height (cm) Change from Baseline to Year 2	NA	TS	1	Major allele presence	0.035523	0.0355	50.0%	100.00%
rs2297141	CYR61	2	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.01827	0.0365	41.5%	95.92%
rs3817899	IGFALS	1	Height (cm) Change from Year 1 to Year 2	NA	TS	1	Genotype	0.039601	0.0396	11.9%	100.00%
rs2278914	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.013613	0.0408	11.0%	97.96%
rs4558548	PPP1CB	12	Height SDS Change from Baseline to Year 2	NA	TS	5	Genotype	0.008478	0.0424	32.1%	100.00%
rs361082	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs361088	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs361059	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs361094	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs497900	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs2197387	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs4305444	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs191775	PIK3CB	23	Height Velocity SDS at Year 2	NA	TS	2	Genotype	0.021381	0.0428	31.0%	100.00%
rs10192250	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.014906	0.0447	10.7%	100.00%
rs1454222	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.014906	0.0447	10.7%	100.00%
rs12471731	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.014906	0.0447	10.7%	100.00%
rs4142729	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.014906	0.0447	10.7%	100.00%
rs1947432	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.014906	0.0447	10.7%	100.00%
rs2290445	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.014906	0.0447	10.7%	100.00%
rs1454225	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Minor allele presence	0.014906	0.0447	10.7%	100.00%
rs751210	SLC2A1	14	Height Velocity SDS at Year 2	NA	TS	8	Minor allele presence	0.00605	0.0484	25.0%	100.00%
rs10192250	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.016291	0.0489	10.7%	100.00%
rs1454222	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.016291	0.0489	10.7%	100.00%
rs12471731	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.016291	0.0489	10.7%	100.00%

TABLE 5-continued

Associated SNPs through Continuous analyses											
SNP ID	Gene	Nb Markers in Gene	Quantitative Variable	Gen- der	Dis- ease	Nb LD Blocks	Association Tested	Nominal p-value	Adjust- ed p-value	Minor Allele Fre- quency	Call Rate
rs4142729	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.016291	0.0489	10.7%	100.00%
rs1947432	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.016291	0.0489	10.7%	100.00%
rs2290445	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.016291	0.0489	10.7%	100.00%
rs1454225	SOS1	49	Height (cm) Change from Year 1 to Year 2	NA	TS	3	Minor allele presence	0.016291	0.0489	10.7%	100.00%
rs357044	LHX4	25	Height (cm) Change from Year 1 to Year 2	NA	TS	21	Minor allele presence	0.002343	0.0492	11.9%	100.00%
rs2168043	SOS1	49	Height (cm) Change from Baseline to Year 2	NA	TS	3	Genotype	0.016436	0.0493	17.9%	100.00%
rs759160	EGFR	48	Height SDS Change from Baseline to Year 2	NA	TS	32	Minor allele presence	0.001558	0.0499	19.0%	100.00%
rs2276048	INPPL1	2	Height (cm) Change from Year 1 to Year 2	NA	TS	1	Major allele presence	0.058758	0.0588	19.0%	100.00%

The invention claimed is:

1. A method of treating an individual having Growth Hor-
mone (GH) Deficiency comprising:
- a) treating the individual having a growth hormone defi-
ciency with growth hormone for a period of two years;
 - b) determining in a DNA sample of the individual whether
in the STAT gene cluster rs2293152 the CC, CG, or GG
genotype is present; and
 - c) administering a daily dose of growth hormone ranging
from about 0.02 mg/kg of body weight to about 0.07
mg/kg of body weight to an individual having the CC
genotype or administering a daily dose of growth hor-
mone, said daily dose being greater than about 0.02
mg/kg of body weight to about 0.07 mg/kg of body
weight, to an individual having the GG or CG genotype.

2. A method of treating an individual having Growth Hor-
mone (GH) Deficiency comprising:

- a) determining in a DNA sample of the individual whether
in the STAT gene cluster rs2293152 the CC, CG, or GG
genotype is present; and
- b) administering a daily dose of growth hormone ranging
from about 0.02 mg/kg of body weight to about 0.07
mg/kg of body weight to an individual having the CC
genotype or administering a daily dose of growth hor-
mone, said daily dose being greater than about 0.02
mg/kg of body weight to about 0.07 mg/kg of body
weight, to an individual having the GG or CG genotype.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 9,206,480 B2
APPLICATION NO. : 14/116355
DATED : December 8, 2015
INVENTOR(S) : Croteau et al.

Page 1 of 1

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In the specification

Column 10,

Line 16, delete “from year to 2 years” and insert --from 1 year to 2 years--.

Column 24,

Line 19, delete “2×2” and insert --2 X 2--.

In the claims

Column 51,

Line 25, claim 1, delete “Deficiency comprising:” and insert
--Deficiency or Turner Syndrome (TS) comprising:--.

Column 52,

Line 25, claim 2, delete “Deficiency comprising:” and insert
--Deficiency or Turner Syndrome (TS) comprising:--.

Signed and Sealed this
Twenty-sixth Day of July, 2016



Michelle K. Lee
Director of the United States Patent and Trademark Office